```
April 18, 2006, 19:11:02 ; Search time 948 Seconds (without alignments).
2398.458 Million cell updates/sec
GenCore version 5.1.7
Copyright (c) 1993 - 2006 Biocceleration Ltd.
                                                                                                                                                                                                                                                                                                                        11766282
                                                                                                                                                                                                     1 agagctgcttggtcagacttatccagattcttggcggtag 40
                                                                                                                                                                                                                                                                                      5883141 seqs, 28421725653 residues
                                                                                                                                                                                                                                                                                                                    Total number of hits satisfying chosen parameters:
                                                               OM nucleic - nucleic search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                         Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                                     IDENTITY NUC Gapop 10.0 , Gapext 0.1
                                                                                                                                                                                                                                                                                                                                                        Minimum DB seq length: 0
Maximum DB seq length: 200000000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GenEmbl:*

1: gb_ba:*

2: gb_ln:*

4: gb_on:*

5: gb_ov:*

6: gb_pat:*

7: gb_ph:*

9: gb_pr:*

10: gb_sts:*

11: gb_sy:*

11: gb_sy:*

13: gb_hn:*

14: gb_hn:*

15: gb_hn:*
                                                                                                                                                                  SEQ3-THEN-SEQ4
40
                                                                                                                                                                  Title:
Perfect score:
Sequence:
                                                                                                                                                                                                                                       Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Database :
                                                                                                                                                                                                                                                                                        Searched:
                                                                                                  Run on:
```

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description		AL391259 Human DNA	AC092268 Homo sapi	AC009292 Homo sapi	AC022254 Homo sapi	BX284653 Homo Bapi	AL049820 Human DNA	BT002723 Arabidops	AY050402 Arabidops	Continuation (4 of	AC099319 Felis cat	AC113932 Homo sapi	AC027298 Mus muscu	AC116992 Homo sapi	AC165609 Bos tauru	AC130715 Mus muscu	AL928713 Mouse DNA	G46487 Z12029 1 Ze	AX536900 Sequence
	Ę	**************************************	AL391259	AC092268	AC009292	AC022254	4 BX284653 0	HSDJ137K2	5 BT002723	5 AY050402	5 CR380948 3	4 AC099319	AC113932	AC027298	AC116992	4 AC165609	AC130715	AL928713	0 G46487	AX536900
	Ę	9 ;	8	æ	æ	œ	7	æ	=======================================	=======================================	12	7	æ	σ	8	14	σ.	6	ដ	•
	Query	Thermal Car	163520	183539	182855	188601	110000	187507	3018	3292	110000	157285	194645	201467	204162	82207	168935	212028	474	2091
æ	Query		63.0	63.0	61.0	61.0	60.5	60.5	58.0	58.0	58.0	58.0	58.0	58.0	58.0	57.5	57.0	57.0	56.5	56.5
	97000	27026	25.2	25.2	24.4	24.4	24.2	24.2	23.2	23.2	23.2	23.2	23.2	23.2	23.2	23	22.8	22.8	22.6	22.6
	Result	2	Н	7	е	4	S	9	7	80	σ	10	11	12	13	14	12	16	11	18
	Re	i	υ	U		U						U	υ			O				

56.5 5403 8 HSW808431 BX648283 Homo sapi 56.5 104024 8 AC005305 AC005305 AC005305 Homo sapi 56.5 104024 8 AC005305 AC005305 AC005305 Homo sapi 56.5 156785 14 AC146517 AC146518 AC005325 Homo sapi 56.5 202568 14 AC146518 AC005325 Homo sapi 56.5 207521 14 AC140518 AC12038 BACHUB no 56.5 277521 14 AC12058 AC121338 Homo sapi 56.0 103068 15 CMS00762 AC121338 Homo sapi 56.0 103060 14 AC009722 AC12038 AC121338 Homo sapi 56.0 153137 8 AC16235 AC00525 Homo sapi 56.0 153137 8 AC00525 AC00525 AC00592 Homo sapi 56.0 153137 8 AC00525 AC00525 AC00527 Homo sapi 56.0 153137 8 AC00525 AC00525 AC00525 AC	Mapp e gro
--	-------------

CDS

gene

FEATURES

CDS

gene

```
regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= 30; an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one subclone; and the assembly was confirmed by restriction digest, except on the rare occasion of the clone being a YAC.

1. 163520
   finished as follows unless otherwise noted: all
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /locus_tag="RP11-469E19.1-001"
/note="match: proteins: AAH51622 F26H11.5 000299 015247
095833 P35526 Q29238 Q9LN39 Q9N2G5 Q9NVF8 Q9NZA1 Q9XSA7
Q9Y696 Q9Z0W7 Q9Z1Q5"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      join(74725. 75199,112561. 112814,118090. 118235, 120547. 120626,123815. 123331,125919. 126112, 129746. 129861,130056. 130301,130383. 130521, 132381. 132381. 133652, 133861. 132381. 132383. 133652, 133861. 132381. 132381. 133765, 137665, 140011. 140147,142038. 142171,151880. 151967, 159862. 155304,156572. 155667,157097. 151967, 151980. 151967, 151980. 151967, 151980. 151967, 151986. 19797,18:2266. 159709,160928. 161048, ALIO9797.18:12262. 12312,ALIO9797.18:132262. 12346,ALIO9797.18:21921. 22029, ALIO9797.18:22262. 22408,ALIO9797.18:21921. 236352, ALIO9797.18:4002. 44267, ALIO9797.18:4023. 3186,ALIO9797.18:361997. 18:4023. 3186,ALIO9797.18:41602. 44267,ALIO9797.18:41802. 44267,ALIO9797.18:418867. 49072,ALIO9797.18:50412. 56622,ALIO9797.18:50712. 56622,ALIO9797.18:50717. 55626,ALIO9797.18:50717. 556249,ALIO9797.18:50717. 55626,ALIO9797.18:50577. 55249,ALIO9797.18:50717. 55626,ALIO9797.18:50577. 652249)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              // Jacob Edg="RP5-1172N10.1-001"
join(74725. 75199.112561. 112814,118090. 118235,
120547. 120626,122815. 12331,125919. 126112,
120547. 120861,120815. 12331,125919. 126112,
123381. 132533,133612. 133716,137459. 137652,
140011. 140147,142038. 142171,151880. 151967,
154962. 155304,156572. 155667,157097, 157308,
159085. 15325,153550. 159709,160228. 161048,
AL109797.18:12187. 12312,AL109797.18:13662. 13787,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /product="ubiquitin specific protease 9, X-linked (fat facets-like, Drosophila)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note="match: ESTB: AA007667.1 AA133380.1 AF197970.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AL109797.18:14979. 15145, AL109797.18:21921. 22029, AL109797.18:2262. 22408, AL109797.18:23034. 23180, AL109797.18:23034. 23180, AL109797.18:23034. 23180, AL109797.18:30973. 31163, AL109797.18:36730. 265950, AL109797.18:30973. 31163, AL109797.18:41569. 42222, AL109797.18:42890. 43013, AL109797.18:44042. 44267, AL109797.18:42890. 43013, AL109797.18:40412. 50632, AL109797.18:50719. 50807, AL109797.18:50719. 50807,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /codon_start=1
/product="chloride intracellular channel 4 (CLIC4)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        5079, AL109797.18:55237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             .56266, AL109797.18:58057
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    66089. ..66840
/locus tag="RP11-469E19.1-001"
/pseudo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /locus_tag="RP5-1172N10.1-001"
                                                                                                                                                                                                                                                                                                                   'organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                        DNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 clone_lib="RPCI-11.2"
                                                                                                                                                                                                                                                                                                                                                 /mol_type="genomic_DN
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                           /map="p11.4-21.2"
/clone="RP11-469E19"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AL109797.18:54923.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AL109797.18:56171.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 66089. .66840
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          'gene="USP9X'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /gene="USP9X
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      facets-like,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           pseudogene"
This sequence was
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /pseudo
                                                                                                                                                                                                                                                                                         source
```

mRNA

LLOGISS FROGENIALISTURING STATEMENT COLORIST CONTROLLS IN COLORIST CONTROLLS IN COLORIST CONTROLLS IN CONTROL /standārd_name="OTTHUMP00000023142" /note="match: proteins: 000507 P70398 Q8C7T5 Q8WWT3 Q8WX12 FPLLELLAMALNPHCKFHIYNGTRPCESVSSSVQLPEDELFARSPDPRSPKGWLVDLL NKFGTLNGFQILHDRFINGSALNVQIIAALIKPFGQCYBFLTLHTVKKYFLPIIEMVP QFLENLTDEELKKGAKNBAKNDALSMIIKSLKNLASRVPGQEETVKNLEIFRLKMILR AYNSNINVPNAEVLLANBIDWLKRIRDDVKRTGETGIEETILEGHLGVTKELLAFQTS EKKFHIGCEKGGANLIKBLIDDFIFPASNVYLQYMRNGELPAEQAIPVCGSPPTINAG FELLVALAVGCVRNIKQIVDSLTEMYYIGTAITTCEALTEWEYLPPVGPRPPKGFVGL /translation="wtattrgspvggndnggqapdggsqpplcqqngtsspdssnensp atppdbggggdappqledbeepapphtdlakklddminrprwvvpvlpkgelevlleaai dlskkgldvksbacqrpprdgltisptkiltdbavsgwkpeihvslvelcvaklsqdw KONAGATCYMNSVI QQLYMI PSIRNGILAI EGTGSDVDDDMSGDEKQDNESNVDPRDDV FGY PQQFEDKPALSKTEDRKEYNI GVLRHLQVI FGHLAASRLQYYVPRGFWKQFRLWG **VRQVAQEQFFLMCTRCCMGHRPLLFFTTLLFTVLGSTARERAKHSGDYFTLLRHLLNY** SEQSESETAGSTKYRLVGVLVHSGQASGGHYYSYIIQRNGGDGERNRWYKFDDGDVTE CKMDDDEEWKNQCFGGBYMGEVFDHMYKRMSYRRQKRWWNAYILFYERMDTIDQDDEL iryiselaittrphoiimpsaiersvrkonvopphinrmoysmeypoprkkllicngvy Lipppogodhilpeaeeitmisiolaarflfttgfhtkkvvrgsasdwydalcillrhs AW608199.1 BE079462 BE694065 BE809565 EPVNLREOHDALEFFNSLVDSLDEALKALGHPAMLSKVLGGSFADOKI CQGCPHRYEC ees pttlinvd i rnhonelds leq yvkgdllegana yhcekcnkkvd tvkrll i kklipf .9798, JOSTON (112719. 112814, 118090. 118235, 120547. 120626, 123815. 123931, 125919. 125112, 129746. 129861, 130805. 159805. 159805 match: CDNA6: AB028980 AF000986 AF070645 U67874 X98296 /product="ubiquitin specific protease 9, X-linked (fat facets-like, Drosophila)"
/protein id="CAD13527.2"
/db_xref="GAI:57209221"
/db_xref="InterPro:IPR001394"
/db_xref="InterPro:IPR001394" AF197971.1 AI097937.1 AI228327.1 AI526622.1 AI761675.1 AJ392219 AW107303.1 AW608199.1 BE(H43281.1 N34148.1 N36287.1 R80323. /locus_tag="RP5-1172N10.1-001" /codon_start=1 /gene="USP9X"

```
KLSVPÄTFMLVSLDEGPGPPTKYQYAELGKLYSVVSÖLTRCCNVSSRMOSSINGNPPL
PNPPGDPNLSQPIMPIQONVADILFVRTSYVKKIIEDCSNSEETVKLLRFCCWENPQF
SSTVLSELLWQVAYSYTYELRPYLDLLLQILLIEDSWQTHRIHNALKGIPDDRDGLFD
                                                                                                                TIORSKAHYORRAYOCIKCMVALFSNCPVAYOILOGNGDLKRKWTWAVEWLGDELERR
PYTGNPQYTYNNWSPPVQSNETSNGYFLERSHSARWTLAKACELCPEEEPDDQDAPDB
HESPPPEDAPLYPHSPGSQYQQNNHVHGQPYTGPAAHHMNNPQRTGQRAQENYEGSEB
                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
KNVRFWFAHNVLFNVSNRFSEYLLECPSAEVRGAFAKLIVFIAHFSLQDGPCPSPFAS
PGPSSQAYDNLSLSDHLLRAVLNLLRREVSEHGRHLQQYFNLFVMYANLGVAEKTQLL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRI 28-JUL-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Buarchontoglires, Primates, Catarrhini,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C (bases I to 183539)
Wen,G. and Platzer,M.
Direct (Submission
Submitted (03-JUL-2001) Genome Analysis, Institute of Molecular
Biotechnology, Beutenberstr. 11, Jena, Thuringia 07745, Germany
Men,G. and Platzer,M.
Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted (26-JAN-2002) Genome Analysis, Institute of Molecular Biotechnology, Beutenbergstrasse 11, Jena 07745, Germany (becchnology, Beutenbergstrasse 11, Jena 07745, Germany (becchnology, and Platzer, M. Direct Submission Submitted (05-AUG-2002) Genome Analysis, Institute of Molecular Biotechnology, Beutenberstr. 11, Jena, Thuringia 07745, Germany (bases 1 to 18353)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AC092268 181539 bp DNA linear PRI 28-JUL-2
Homo sapiens chromosome X clone RP11-185017 map p11.4, complete
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (28-JUL-2004) Genome Analygis, Institute of Molecular Biotechnology, Beutenbergstrasse 11, Jena 07745, Germany On Jul 28, 2004 this sequence version replaced gi:22095403.
                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Wen,G., Ramser,J., Blechschmidt,K., Meindl,A. and Platzer,M. Unpublished
                                                                                                                                                                                                                                                                                                                                                                              Score 25.2; DB 8; Length 163520; Pred. No. 23; 0; Mismatches 3; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequencing vector: M13mp18; 100% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Center: Institute of Molecular Biotechnology
                                                                                                                                                                                                           join[156235. .156667,157097. .157306)
/gene="USP9X"
                                                                                                                                                                                                                                                             /iocus_tag="RP5-1172N10.1-002"
join(156232..15667,157097..157306)
/gene="USP9X"
/locus_tag="RP5-1172N10.1-002"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Web site: http://genome.imb-jena.de/
Contact: gscj-submit@genome.imb-jena.de
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 20183 GAGCTGCTTGGTCAGACTTCTCCACAATCT 20154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Center project name: X144
Center clone name: RP11-185017
----- Summary Statistics
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2 GAGCTGCTTGGTCAGACTTATCCAGATTCT 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AC092268.4 GI:50726746
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (bases 1 to 183539)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Center code: IMB
                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 90.0%;
Matches 27; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens (human)
                                                                                                                                                                                            VSPPQTKDQ"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ното варіеля
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AC092268/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REFERENCE
AUTHORS
TITLE
JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REFERENCE
AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TITLE
JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AUTHORS
TITLE
JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REFERENCE
AUTHORS
TITLE
JOURNAL
                                                                                                                                                                                                                     gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AUTHORS
                                                                                                                                                                                                                                                                                           mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMMENT
```

셤 8

```
This sequence was finished as follows unless otherwise noted: all regions were double stranded, sequenced with an alternate chemistry, or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats, all regions were covered by at least one plasmid subclone or more than one subclone.
                                                                                                                                                                                                                                                                                                                                                                             Sequence Quality Assessment:
This entry has been annotated with sequence quality estimates computed by the Phrap assembly program.
All manually edited bases have been reduced to quality zero. Base-by-base quality values are not generally visible from the GenBank flat file format but are available as part of this entry's ASN.1 file.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /uganism=-mondach DNA"
/db_xref="taxon:9606"
/db_xref="taxon:9606"
/db_xref="taxon:9606"
/note="worslapping clone"
6224. 6294
/note="single stranded/single chemistry region"
83209. 83236
/note="single stranded/single chemistry region"
86278. 86287
/note="single stranded/single chemistry region"
89410. 99425
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              128792. .128865
/note="single stranded/single chemistry region"
130343. .13053/
/note="single stranded/single chemistry region"
130485. .131547
/note="pcr product sequence only"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note="pcr product sequence only"
93609 .93618
/note="single stranded/single chemistry region"
100862 .101479
/note="single stranded/single chemistry region"
101954 .102136
/note="single stranded/single chemistry region"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            104000. .104002

/note="low quality region"

/note="single clone coverage"

104906. .104938

/note="single stranded/single chemistry region"

105811. .106634

/note="single stranded/single chemistry region"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note="single stranded/single chemistry region"
90394. .90417
                    040
030
030
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               117448. 117452
/note="Bingle stranded/Bingle chemistry
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   111844. .111882
/note="single stranded/single chemistry
version 0.990329
                  Consensus quality: 183456 bases at least Consensus quality: 183530 bases at least Consensus quality: 183539 bases at least
                                                                                                                                                                                                                                                                                                                      Neighboring sequence information:
This clone is overlapped by RP11-77G22.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1. .77611
/organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          'organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /mol_type="genomic_DNA"
/db_xref="taxon:9606"
                                                                                               Quality coverage: 10.93x
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /clone="RP11-185017"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /chromosome="X"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /map="p11.4"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                .183539
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    nisc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bource
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FEATURES
```

```
Chazaro, B., Choepel, Y., Colangelo, M., Collins, S., Collymore, A., Cook, A., Cooke, P., DeArellano, K., Dewar, K., Diaz, J.S., Dodge, S., Faro, S., Ferreitara, P., FitzHugh, W., Gage, D., Galagan, J., Gardyna, S. Ginde, S., Gord, S., Goyette, M., Graham, L., Grand-Pierre, N., Hagos, B., Horton, L., Hulme, W., Iliev, I., Johnson, R., Jones, C., Kamat, A., Karatas, A., Kells, C., LaRocque, K., Lamazares, R., Landers, T., Lehoczky, J., Levine, R., Lindblad-Toh, K., Liu, G., Macdean, C., Macdonald, P., Major, J., Marquis, N., Matthews, C., McCarthy, M., McEwan, P., McKernan, K., Meldrim, J., Meneus, L., Minow, T., Mengay, V., Murphy, T., Naylor, J., Moyen, C., Nicol, R., Norbu, C., Norman, C.H., O'Connor, T., O'Donnell, P., O'Neil, D., Oliver, J., Peterson, K., Phunkhang, P., Pierre, N., Pollara, V., Roman, G., Retera, R., Rieback, M., Riley, R., Rise, C., Rogov, P., Roman, J., Rosetti, M., Roy, A., Santos, R., Schuer, S., Schupback, Serauss, N., Subramanian, A., Talamas, J., Tesfaye, S., Theodore, J., Topham, K., Travers, M., Trigilio, J., Vassiliev, H., Vol, A., Wilse, M., Xi, Wyman, D., Ye, W.J., Young, G., Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (05-APR-2002) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA & Submitted (05-APR-2002) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA & (bases 1 to 182855)

Birren, B., Linton, L., Nusbaum, C., Lander, E., Ali, A., Allen, N., Anderson, S., Barna, N., Bastien, V., Bloom, T., Boguslavkiy, L., Boukhgalter, B., Brown, A., Camarata, J., Campopiano, A., Chang, J., Cokaraco, B., Choepel, Y., Colangelo, M., Collins, S., Collymore, A., Cook, P., DeArellano, K., Dewar K., Diaz, J.S., Dodge, S., Goyette, M., Graham, L., Grand-Pierre, N., Ginde, S., Goyette, M., Graham, L., Grand-Pierre, N., Hagos, B., Horton, L., Hulme, W., Iliev, I., Johnson, R., Jones, C., Kamat, A., Karatas, A., Kalate, W., Marchew, C., Macdonald, P., Mayor, I., Johnson, R., Machan, P., McCarthy, M., McEwan, P., McGarthy, M., McEwan, P., McGarth, M., Malum, C., Norman, C.H., O'Connor, T., O'Donnell, P., O'Neil, D., Oliver, J., Peterson, K., Phurkhang, P., Peterson, K., Patra, R., Rieback, M., Riley, R., Rise, C., Rogov, P., Raymond, C., Retta, R., Rieback, M., Riley, R., Rise, C., Rogov, P., Sewery, P., Spencer, B., Schauer, S., Schupback, R., Severy, P., Spencer, B., Schupback, R., Viel, 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Web site: http://www-seq.wi.mit.edu
Contact: sequence_submissions@genome.wi.mit.edu
------ Project_Information
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /map="15"
/clone="RP11-34F13"
/clone_lib="RPCI-11 Human Male BAC"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /mol_type="genomic_DN
/db_xref="taxon:9606"
/chromosome="15"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Center clone name: 34_F_13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      17. .1452
/rpt_family="L1MEC"
1479. .1694
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Center project name:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Center code: WIBR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REFERENCE
AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TITLE
JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Barren, B., Linton, L., Nusbaum, C., Lander, E., Allen, N., Anderson, M., Barren, B., Linton, L., Nusbaum, C., Lander, E., Allen, N., Anderson, M., Baker, J., Baldwin, J., Barna, N., Beckerly, R., Benn, J., Brown, A., Castle, A., Cerny, J., Colangelo, M., Collins, S., Collymore, A., Cooke, P., DeArellano, K., Depayre, E., Devon, K., Dewar, K., Cooke, P., DeArellano, K., Depayre, E., Devon, K., Dewar, K., Cooke, P., Grant, G., Funke, R., Gage, D., Galagan, J., Gardyna, S., Gilbert, D., Grant, G., Hagos, B., Heaford, A., Horton, L., Howland, J.C., Jones, C., Kann, L., Karatas, A., Lehorczky, J., Lieu, C., Locke, K., Macdonald, P., Marquis, N., McEwan, P., McEwarn, K., McLaughlin, J., Mardiff, M., O'Connor, T., O'Donnell, P., Pavilin, B., Peterson, K., Pollara, V., Riley, R., Roberts, D., Roy, A., Severy, P., Stange-Thomann, N., Stojanovic, N., Stone, C., Subramanian, A., Tesfaye, S., Torruella-Miller, I., Vassiliev, H., Vo, N., Wagner, A., Wheeler, J., Wu, X., Wyman, D., Ye, W.J. and Zody, M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRI 14-MAY-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Buarchontoglires, Primates, Catarrhini,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (13-AUG-1999) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ACO09292 182855 bp DNA linear PRI 14-MAY-2
Homo sapiens chromosome 15, clone RP11-34F13, complete sequence.
ACO09292
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3 (bases 1 to 182855)
Birren, B., Linton, L., Nusbaum, C., Lander, E., Ali, A., Allen, N., Anderson, S., Barna, N., Bastien, V., Bloom, T., Boguslavkiy, L., Boukhgalter, B., Brown, A., Camarata, J., Campopiano, A., Chang, J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                            /note="low quality region"
131695. 132029
/note="single stranded/single chemistry region"
134563. 134703.
134880. 134990
                                                                                                                                                                                                                                                                                                                                                                                                                        148458. 148492
/note="single stranded/single chemistry region"
149777. 149830
150033. 150066
/note="single clone coverage"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      63.0%; Score 25.2; DB 8; Length 183539; 90.0%; Pred. No. 23; ive 0; Mismatches 3; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    'note="single stranded/single chemistry region"
                                                                                                                                                                                                                                                                                                                                                                                               'note="single stranded/single chemistry region'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Hominidae, Hono

1 (bases 1 to 182855)

Birren, B., Linton, L., Nusbaum, C. and Lander, E.

Homo sapiens chromosome 15, clone RP11-34F13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           174548 GAGCTGCTTGGTCAGACTTCTCCACAATCT 174519
                                                                                131258. .131259
/note="low quality region"
131341. .131343
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2 GAGCTGCTTGGTCAGACTTATCCAGATTCT 31
                                                    'note="low quality region"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       'note="low quality region"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    150339. .150440
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AC009292.11 GI:20564447
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens (human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity 90.0
Matches 27; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           156678
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       156678
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  misc_feature
                     misc_feature
                                                                                        misc_feature
                                                                                                                                                       misc_feature
                                                                                                                                                                                                                          misc_feature
                                                                                                                                                                                                                                                                                             misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                   misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ungure
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 3
AC009292
LOCUS
DEFINITION
ACCESSION
VBRSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOURCE
ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AUTHORS
TITLE
JOURNAL
REFERENCE
AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             KEYWORDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ORIGIN
```

δ

```
/ ref. family="Miss" complement (20915. 21128) / ref. family="Miss" complement (20915. 21128) / ref. family="L2" / ref. family=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          / rpt_cmm:r (13864. .14165)
/ rpt_family="AluSx"
/ rpt_family="MIR"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /rpt_family="MIR"
19286. .19435
/rpt_family="MERSA"
complement (19928. .20065)
/rpt_family="FLAM_C"
20583. .20734
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /rpt_family="La"
complement(17335. .17494)
/rpt_family="MER5A"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     rpt family="max.o.n.
:omplement(12203. .12247)
/rpt_family="L2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       12372. .12677
/rpt_family="AluSp"
complement(12933. .13167)
/rpt_family="MIR"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    omplement (17004. .17062)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              rpt family="L2"
complement (13612. 13725)
/rpt_family="MIR3"
                                                                                                                                                                                                                                                                                                                                                                                                           4904 . 4935 / rpt family . 4904 . 4935 / rpt family . (CATA) n" complement (5583. 5805) . frpt family . MBR30" complement (5928. 6047) / rpt family . 12" complement (6215. 6510)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /rpt_fam1+,
16201. .16220
/rot_family="(TTTTG)n"
                                                                                                                                                                                                                                                complement (3452. .4098) / rpt family="L2"
                                                                                                                                                                                                                                                                                                        complement (4319. .4528)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                complement (6831. .6955)
/rpt_family="L2"
5997. .7070
                                                                                                                                                                                                                                                                                                                                                                                          rpt_family="FLAM_A"
904_ 4935
                                                                                                      /rpt_family="Alusx" 2678. .2770 /rpt_family="LIME1" 3167. .3279
/rpt_family="MBR58A"
1695._.1960
                       1695. . 1960
/rpt_family="L1MEc"
2007. . 2320
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            family="AluSx"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /rpt_family_
18647. .18820
/rpt_family="MIR"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   'L1PA3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                family="L1MC4"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /rpt_family="AluSp"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 .7070
family="MIR"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "MIR"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           family="MIR"
                                                                                                                                                                                                                         'rpt family="L2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   family="M
8. .17996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        18554
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         .10945
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               rpt_family="17559..17803
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               rpt_family="
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   family=
                                                                                                                                                                                                                                                                                                                                                             .4903
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      8448. ..
                             repeat_region
                                                                                     repeat_region
                                                                                                                                         repeat_region
                                                                                                                                                                                              repeat_region
                                                                                                                                                                                                                                                      repeat_region
                                                                                                                                                                                                                                                                                                              repeat_region
                                                                                                                                                                                                                                                                                                                                                                     repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                             repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    repeat_region
```

```
23 (Dases 1 to 188601)

Anderson, S., Baldwin, J., Barna, N., Beckerly, R., Beda, F., Anderson, S., Baldwin, J., Barna, N., Beckerly, R., Beda, F., Anderson, S., Baldwin, J., Barna, N., Burkett, G., Castle, A., Choepel, Y., Colangelo, M., Collins, S., Collymore, A., Cooke, P., DeArellano, K., Dewar, K., Donino, M., Doyle, M., Penestor, J., Garthao, K., Dewar, K., Domino, M., Doyle, M., Penestor, J., Ferreira, P., FitzHugh, W., Forrest, C., Gage, D., Galagan, J., Gardyna, S., Grant, G., Hagos, B., Heaford, A., Horton, L., Klein, J., Landers, T., Lehoczky, J., Levine, R., Lieu, C., Liu, G., Locke, K., McPheeters, R., Medrain, J., McChan, P., McGurk, A., McKernan, R., McPheeters, R., Meldrim, J., Meneus, L., Morton, L., McPheeters, R., McDani, J., Morton, J., Norman, C.H., O'Connor, T., O'Donnell, P., Olivar, T.M., Peterson, K., Pierre, N., Fiston, S., Santos, R., Severy, P., Spencer, B., Stange-Thomann, N., Santos, R., Severy, P., Spencer, B., Stange-Thomann, N., Stojanovic, N., Subramailan, A., Talamas, J., Tesfaye, S., Theodore, J. Tirrell, A., Vashilev, H., Viel, R., Vo, A., Wu, X., Wyman, D., Ye, W. J., Zimmer, A. and Zody, M.

Submitted (27-JAN-2000) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, Ma 02141, USA

Birren, B., Nusbaum, C., Lander, E., Ali, A., Allen, N., Anderson, S., Camarata, J., Chang, J., Graham, L., Gard, S., Geraham, L., Gard, S., Geraham, L., Gard, P., Landers, T., Levine, R., Lindblad-Toh, Karatas, A., Karatas, A., Karatas, J., Hulme, W., Illey, T., Levine, R., Lindblad-Toh, Karatas, A., Karatas, J., Liley, T., Levine, R., Lindblad-Toh, Karatas, J., Chang, T., Liley, T., Levine, R., Lindblad-Toh, Karatas, J., Chang, J., Liley, T., Levine, R., Liley, T., Levine, T., Lindblad-Toh, Karatas, J., Chang, T., Liley, T., Levine, T., Liley, L., Landers, T., Levine, T., Landers, T., Liley, L., Landers, T., Landers, T., Landers, T., 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AC022254 188601 bp DNA linear PRI 20-JUL-2002
Homo sapiens chromosome 15, clone RP11-282M16, complete sequence.
AC022254
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Buarchontoglires; Primates; Catarrhini;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61.0%; Score 24.4; DB 8; Length 182855; 82.4%; Pred. No. 47; ive 0; Mismatches 6; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Hominidae, Homo.

1 (bases 1 to 188601)

Birren,B., Nusbaum,C. and Lander,E.
Homo sapiens chromosome 15, clone RP11-282M16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     112933 CTGCTTGTTCAGATTTATCCACATGCTTGCCAGT 112966
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     5 CTGCTTGGTCAGACTTATCCAGATTCTTGGCGGT 38
                                                                                                      /rpt family="AluJo"
complement (24.77. .24301)
/rpt family="FLAM A"
complement (25.715. .25831)
/rpt family="FLAM A"
complement (36.74. .26479)
/rpt family="AluSx"
/rpt family="AluSx"
/rpt family="AluSx"
/rpt family="AluSx"
/rpt family="AluSx"
                            /rpt_family="L2"
complement(21849. .21903)
/rpt_family="L2"
complement(22600. .22890)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AC022254.11 GI:21913035
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (bases 1 to 188601)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens (human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 82.4<sup>3</sup>
Matches 28; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Unpublished
repeat_region
                                                         repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              repeat_region
                                                                                                                      repeat_region
                                                                                                                                                                                   repeat_region
                                                                                                                                                                                                                                                repeat_region
                                                                                                                                                                                                                                                                                                          repeat_region
                                                                                                                                                                                                                                                                                                                                                                       repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                    repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AC022254/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REFERENCE
AUTHORS
TITLE
JOURNAL
REFERENCE
AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TITLE
JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REFERENCE
AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Locus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ద
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ઠે
```

```
repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          repeat_region
                                                                                 repeat_region
                                                                                                                                            repeat_region
                                                                                                                                                                                                              repeat_region
                                                                                                                                                                                                                                                                         repeat_region
                                                                                                                                                                                                                                                                                                                                       repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                  repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            repeat_region
                                                                                                                                                                                                                                                                                                                                                 Direct Submates 1202) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA Research, 320 Charles Street, Cambridge, MA 02141, USA Research, 320 Charles Street, Cambridge, MA 02141, USA Barren, B. Nusbaum, C., Lander, E., Ali, A., Allen, N., Anderson, S., Barren, B., Nusbaum, C., Lander, E., Ali, A., Allen, N., Anderson, S., Cook, A., Cooke, P., DeArellano, K., Dewar, K., Diaz, J.S., Dodge, S., Faro, S., Faro, S., Faro, S., Gord, S., Graham, L., Grand-Pierre, N., Hagos, B., Horton, L., Hulme, W., Illev, I., Johnson, R., Lindblad-Toh, K., Liu, G., MacLean, C., Macdonald, P., Major, J., Matthews, C., Karats, A., MacLean, C., Macdonald, P., Major, J., Matthews, C., Murphy, T., Naylor, J., Nicol, R., Norbu, C., Norman, C., Phunkhang, P., Plerre, N., Raymond, C., Retta, R., Rise, C., Rogov, P., Roman, J., Roy, A., Schauer, S., Schubback, R., Steganan, S., Severy, P., Smith, C., Spencer, B., Stange-Thoman, N., Stojanovic, N., Talamas, J., Tesfave, S., Theodore, J., Topham, K., Travers, M., Vassiliev, H., Zambek, L., Zimmer, A. and Zody, M., Wilson, B., Wyman, D., Young, G., Zainoun, J., Zembek, L., Zimmer, A. and Zody, M., Wilson, B., Wyman, D., Young, G., Zainoun, J., Zembek, L., Zimmer, A., Anderson, M., Wilson, B., Wyman, D., Young, G., Zainoun, J., Zembek, L., Zimmer, A. and Zody, M., Wilson, B., Wyman, D., Young, G., Zainoun, J., Zembek, L., Zimmer, A., Wilson, B., Wyman, D., Young, G., Zainoun, J., Zembek, L., Zimmer, A., Wilson, B., Wyman, D., Young, G., Zainoun, J., Zembek, L., Zimmer, A., Wilson, B., Wyman, D., Young, G., Zainoun, J., Zembek, L., Zimmer, A., Wilson, B., Wyman, D., Young, G., Zainoun, J., Zembek, L., Zimmer, A., Wilson, B., Wyman, D., Young, G., Zainoun, J., Zembek, L., Zimmer, A., Wilson, B., Wyman, D., Young, G., Zainoun, J., Zembek, L., Zimmer, A., Wilson, B., Wyman, D., Young, G., Zainoun, J., Man, Wilson, B., Wyman, J., Wyman, D., Wyman, D., Wyman, J., Wyman,
Liu, G., MacLean, C., Macdonald, P., Major, J., Matthews, C., McCarthy, M., Meldrim, J., Meneus, L., Mihova, T., Mlenga, V., Murphy, T., Naylor, J., Nguyen, C., Nicol, R., Norbu, C., Norman, C.H., O'Connor, T., O'Donnell, P., O'Neil, D., Oliver, J., Peterson, K., Phunkhang, P., Pierre, N., Raymond, C., Retta, R., Rise, C., Rogov, P., Roman, J., Roy, A., Schauer, S., Schupback, R., Seaman, S., Severy, P., Smith, C., Spencer, B., Stange-Thoman, N., Stojanovic, N., Talamas, J. Tesfaye, S., Theodore, J., Topham, K., Travers, M., Vassiliev, H., Zembek, L., Zimmer, A. and Zody, M., Wyman, D., Young, G., Zainoun, J., Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted (20-JUL-2002) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA On Jul 20, 2002 this sequence version replaced gi:21591923. All repeats were identified using RepeatMasker: Smit, A.F.A. & Green, P. (1996-1997) http://ftp.genome.washington.edu/RM/RepeatWasker.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              .----- Genome Center Center for Genome Research Center: Whitehead Institute/ MIT Center for Genome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /clone="RP11-282M16"
/clone lib="RPCI-11 Human Male BAC"
275. .351
/rpt family="(TA)n"
/complement(852. .1154)
/rpt_family="AluJb"
/rpt_family="AluJb"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1155. 1414
/rpt_family="LIME4A"
1417. 1439
/rpt_family="(TG)n"
complement(1449. 1607)
/rpt_family="LIMC4"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
/chromosome="15"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        complement (2999. .3294)
/rpt_family="AluJo"
3489. .3630
/rpt_family="LTR54"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 family="HAL1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Center code: WIBR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /map="15'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TITLE
JOURNAL
                                                                                                                                                                                                                                                                                                                                    TITLE
JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                               REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMMENT
```

```
/rpt_family="L1MB7"
complement(5045. .5207)
/rpt_family="FAM"
5208. .5424
                                                                                                                                                                                                                                                                                        7883. . 7949

/rpt family="(TG)n"

complement (7951. . 8247)

/rpt family="Alusx"

complement (8248. . 8550)

/rpt family="Aludo"

complement (8646. . 9063)

/rpt family="MLTIJ1"

9236. . 9331
                                                                                                                                                                                /rpt_family="LlMB7"
complement(5779. .6070)
/rpt_family="AluSg"
6087. .6435
/rpt_family="LlMB3"
complement(7060. .7479)
                                                                                                                                                                                                                                                      /rpt_family="MSTB" 7883. .7949
                                                                                                                 /rpt family="LIMB7"
complement (5425. .5719)
/rpt family="AluJb"
5720. .5776
                                                                                                                                                                                                                                                                                                                                                                                                                                /rpt family="FLAM A"
complement (9603. _9929)
/rpt family="MLT1C"
10093. .11120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /rpt_family="AT_rich"
11810. .11871
/rpt_family="AT_rich"
11901. .12054
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          'rpt family="AluSg/x" (6800 . 17070
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             rpt_family="L1ME4A"
1311. .11549
rpt_family="L1ME4A"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /rpt family="LIMB7"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  rpt_family="L1MB4A"
2466. .12509
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /rpt_family="LIMB7"
14133. .14190
/rpt_family="LIMC2"
14191. .14218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /rpt_family="AluJb"
16411. .16637
/rpt_family="LIMB7"
16639. .16799
              . .444<u>2</u>
_family="LTR54"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         rpt_family="AluSx"
|5587. .16115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       rpt family="L1MB7"
7556. .17762
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /rpt_family="AluJo"
18092. .18275
rpt_family="LOR1b"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       rpt_family="AluJb"
4503. .15255
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        rpt_family="L1MB7"
4219. .14502
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     rpt_family="L1MB7"
5256. .15586
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               rpt_family="MIR3"
3960. .14132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /rpt_family="MIR"
17772. .18080
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  rpt_family="MIR"
2624. .12742
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             rpt_family="I
1614. .11644
                                           .5044
```

8

```
HSDJ137K2 18-MAY-2005
Human DNA sequence from clone RP1-137K2 on chromosome 6q25.1-25.3
Contains part of the gene for BRG1-binding protein BLD/OSA1 (p250R KTAA1235) (FLJ00253 FLJ22292), a novel gene and two CpG islands, AL049820
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bukaryota; Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Buarchontoglires, Primates, Catarrhini,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AL049920.23 GI:8247261
HTG; CpG island; ELD/OSA1; FLJ00253; FLJ22292; KIAA1235; P250R.
HOmo sapiens (human)
Home sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Сарв
   arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 60.5%; Score 24.2; DB 14; Length 110000; Best Local Similarity 78.4%; Pred. No. 60; Matches 29; Conservative 0; Mismatches 8; Indels 0;
                                                                                        23513 GTTGCTTGTTCAAAATTACCAAGACTCTTGGCAGTAG 23549
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            . . 2085
note="assembly_fragment:00828"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2186. .5001
/note="assembly_fragment:04673"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   5102. .7187

/note="assembly_fragment:08375"

7288. .98390

/note="assembly_fragment:09028"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   101110. .103915 // hote="assembly_fragment:11482"
104016. .135980
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note="assembly_fragment:11565"
136081. .520332_/note="assembly_fragment:11639"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
/chromosome="6"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /clone="XXyac-830B11"
/clone_lib="CEPH"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 (bases 1 to 187507)
Sycamore, N.
Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Hominidae; Homo
                                                                                                            2086
2186
5002
5002
5102
7188
98391
98491
101010
101110
104016
1135981
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LOCUS
DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 6
HSDJ137K2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AUTHORS
TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REFERENCE
                                                                                                                                                                                                                                                                                                                                                                               FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ð
                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    520332 bp DNA linear HTG 14-JUN-2005 e 6 clone XXyac-830B11, WORKING DRAFT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted (13-JUN-2005) Wellcome Trust Sanger Institute, Hinxton, Cambridgeshire, CB10 1SA, UK. B-mail enquiries: vega@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk On Sep 25, 2003 this sequence version replaced gi:35209214.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Buarchontoglires; Primates; Catarrhini;
                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BX284653.17 GI:35763555
HTG; HTGS PHASEL; HTGS_ACTIVEFIN; HTGS_DRAFT; HTGS_FULLTOP.
Homo sapiens (human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    * NOTE: This is a 'working draft' sequence. It currently consists of 8 contigs. The true order of the piece is is not known and their order in this sequence record is
                                                                                                                                                                                                       61.0%; Score 24.4; DB 8; Length 188601; 82.4%; Pred. No. 47; ive 0; Mismatches 6; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                     LOCUS BX284653 Accession BX284653
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Insert size: 519632; sum-of-contigs
Quality coverage: 11.98x in Q20 bases; sum-of-contigs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Assembly program: MGAP4; version 4.5
Sequencing vector: M13; M77815; 7% of reads
Sequencing vector: plasmid; L08752; 92% of reads
Chemistry: Dye-primer-amersham; 1% of reads
Chemistry: Dye-primer Big Dye; 0% of reads
Chemistry: Dye-terminator; 79% of reads
Chemistry: Dye-terminator Big Dye; 0% of reads
Consensus quality: 513402 bases at least Q40
Consensus quality: 514747 bases at least Q20
Consensus quality: 515755 bases at least Q20
                                                                                                                                                                                                                                                                                                         184185 CTGCTTGTTCAGATTTATCCACATGCTTGCCAGT 184152
                                                                                                                                                                                                                                                                                    5 CTGCTTGGTCAGACTTATCCAGATTCTTGGCGGT 38
/rpt_family="(GAAA)n"
complement(18499. .18567)
/rpt_family="MER112"
complement(18568. .18898)
/rpt_family="AluJb"
complement(18898. .19088)
/rpt_family="MER112"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Web site: http://www.sanger.ac.uk
Contact: vega@sanger.ac.uk
------ Project Information
Center project name: yM830B11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          --- Summary Statistics
                                                                                                                                                  /rpt_family="(CA)n"
20265. .20430
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         210000
310000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              410000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens chromosome 6 closEQUENCE, 8 unordered pieces
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      110000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    520332
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Hominidae; Homo.
1 (bases 1 to 520332)
                                                                                                                                                                                                                                                                                                                                                                                                                                     fragments
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       100001
200001
300001
400001
500001
                                                                                                                                                                                                                                               28; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Begin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Center code: SC
                                                                                                                                                                                                          Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence split into 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sycamore, N.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BX284653
                                                                                                                                                                                                                                                                                                                                                                                                                                                Fragment Name
BX284653 0
BX284653 1
BX284653 2
BX284653 2
BX284653 3
BX284653 3
                       repeat_region
                                                                                                                                     repeat_region
                                                                                                                                                                        repeat_region
                                                           repeat_region
                                                                                                repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BX284653
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LOCUS
DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           VERSION
KEYWORDS
SOURCE
ORGANISM
                                                                                                                                                                                                                                               Matches
                                                                                                                                                                                                                                                                                                                                                                           RESULT 5
BX284653 0
WPCOMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REFERENCE
AUTHORS
TITLE
JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMMENT
```

ö

```
CDS
                 Cambridgeshire, CB10 1SA, UK. B-mail enquiries: vega@sanger.ac.uk
Clone requests: clonerequest@sanger.ac.uk
On Jun 4, 2000 this sequence version replaced gi:8018160.
The following abbreviations are used to associate primary accession
numbers given in the feature table with their source databases:
Bm:, BMEL, SW:, SMISSPROT; Tr:, TREMBL; Wp:, WORMPEP; Information
on the WORMPEP database can be found at
http://www.sanger.ac.uk/Projects/C elegans/wormpep This sequence
was generated from part of bacterial clone contigs of human
chromesome 6, constructed by the Sanger Centre Chromosome 6 Mapping
Group. Further information can be found at
http://www.sanger.ac.uk/HGP/Chr6
http://www.sanger.ac.uk/HGP/Chr6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one subclonne; and the assembly was confirmed by restriction digest, except on the rare occasion of the clone being a YAC. RP1-137K2 is from the library RPCI-1 constructed by the group of Pittp://www.chori.org/bacpac/home.htm
Submitted (13-MAY-2005) Wellcome Trust Sanger Institute, Hinxton,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      name="OTTHUMP00000017478"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   'note="Clone_left_end: RP1-137K2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /proteIn_id="CAI42304.1"
/db_xref=="G1:57208441"
/db_xref=="GOA:Q5U46"
/db_xref="InterPro:IPR001606"
/db_xref="UniProt/TrEMBL:Q5JU46"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /organism="Homo sapiens"
| mol Lype="genomic DNA"
| db xref="RZPD:RPC1P704K02137"
| db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                    Center: Wellcome Trust Sanger Institute
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1ocus tag="RP11-419L10.1-004"
                                                                                                                                                                                                                                                                                                                                                                              site: http://www.sanger.ac.uk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /map="q25.1-25.3"
/clone="RP1-137K2"
/clone_lib="RPCI-1"
                                                                                                                                                                                                                                                                                                                                                                                                           Contact: vega@sanger.ac.uk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /chromosome="6"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1, .187507
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /standard
                                                                                                                                                                                                                                                                                                                                                            Center code: SC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               source
JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PEATURES
                                                                     COMMENT
```

```
g
MTPNAR PYQQQUSMDDWGGTFUGAN THOUGH THE STATEMENT OF STATEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Cheuk, R., Chen, H., Kim, C.J., Shinn, P., Bowser, L., Carninci, P., Chan, M., Chang, C.H., Dale, J.M., Hayashizaki, Y., Hsuan, V.W., Ishida, J., Jones, T., Kamiya, A., Karlin-Neumann, G., Kawai, J., Lam, B., Lee, J.M., Lin, J., Miranda, M., Narusaka, M., Narusaka, M., Onodera, C.S., Palm, C.J., Quach, H.L., Sakurai, T., Satou, M., Seki, M., Southwick, A., Tang, C.C., Toriumi, M., Wong, C., Wu, H.C., Yamada, K., Yu, G., Yuan, S., Shinozaki, K., Davis, R.W., Theologis, A. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NPVCREMSMALLSNILAQGDALAARAIAVQKGSIGNLISFLEDGVTMAQYQQSQHNLMH
MQPPPLEPPSVDMMCRAAKALLAMARVDENRSEFLLHEGRLLDISISAVLNSLVASVI
CDVLFQIGQL"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BT002723 318 bp mRNA linear PLN 23-DEC-2002 Arabidopsis thaliana At1g12930/F13K23_14 gene, complete cds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        translation="SQEGYGTRSQPPLAPGKPNHEDLNLIQQERPSSLPDLSGSIDDL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Arabidopsis thaliana
Wakaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, eudicotyledons, core eudicotyledons,
rosids, eurosids II, Brassicales, Brassicaceae, Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Cheuk, R., Chen, H., Kim, C.J., Shinn, P., Bowser, L., Carninci, P.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    join(AL162578.13:<141231. .141336,91557. .91800,
117367. .117456,139935. .140102,155519. .159299)
/gene="RP11-419110.1"
/locus tage="RP11-419110.1-002"
join(AL162578.13:<141231. .141336,91557. .91800,
117367. .117456,139935. .140102,155519. .159299)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /locus_tag="RP11-419110.1-002"
/note="match: CDNAs: AKO74180: 1.0016.
// COMIGLIGEST98.13:<141231. .141336,91557. .91800,
/l17367. .117456,139935. .140102,155519. .155907)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 8; Length 187507;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          8; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 170354 Grigcingricaaaarraccaagacrcriggcagrag 170390
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              name="OTTHUMP00000017477"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GCTGCTTGGTCAGACTTATCCAGATTCTTGGCGGTAG 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         proteIn id="CA142306.1"
/db xref="G1:57208443"
/db_xref="Uniprot/TrEMBL:Q5JU45"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /locus_tag="RP11-419L10.1-002"
/standard_name="OTTHUMP00000017
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 24.2; DB Pred. No. 56; 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FLI CDNA.
Arabidopsis thaliana (thale cress)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /gene="RP11-419L10.1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BT002723.1 GI:27363439
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Arabidopsis ORF clones
Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       tery Match 60.5%; st Local Similarity 78.4%; tches 29; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (bases 1 to 3018)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (bases 1 to 3018)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BT002723
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LOCUS
DBFINITION
ACCESSION
VERSION
KEYWORDS
SOUNCE
ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TITLE
JOURNAL
REFERENCE
AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BT002723
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ઠ
```

```
/product = "AAC11639.1"
/product = "AAC11639.1"
/protein_id="AAC11639.1"
/db_rref="GI_3346"
/db_rref="GI_3346"
/crenslation="MELQRKVAEAHVLNHDPESSNRVAANOWLVOFOLTPAAMDVST
SLLTSPIVSLFDLOFPAAQILERKIONEASHIQSTAKDALLNALLLAAKRYSSGVPQL
ITQICLALSALLLHSDPVSKFPDKLAFALONLQAHDDGNVVLLELLTVLPEBESGDTRH
FSHHSDLROBLLSHTSMVLDPLLQOSENQFVSPLYPHDNNRXILRCLLSWVRAGCFSE
ITQICLALSALLLHSDPVSKFPDKLAFALONLVELVTRHEDLEOVLLYKVOFLENTLK
FALINADLKIISGLSHTSMVLDFLLOQSENQFVSPLYPHDNNRXILRCLLSWVRAGCFSE
IPQGAVFSHPLLNYVFNALGGTTPDLAISVTRLFDFPDKAFNTARDLEOVLLYKROFLENTLK
PALINADLKIISGLACHRONTGTPLPVSKLFFGGVPSSSVSMPLREIBALDF
GLDLPDGLLHFRNNLLELLVDICQLLHPTTYVSKLFFGGVPSSSVSWPLREIBAKLFA
GLDLPDGLLHFRNNLLELLVDICSRACASALRKIICEDAPAVIQBTSNLDILMMIGECLE
VPPSNARPLLLFLAGGISSPICSRACASALRKIICEDAPAVIQBTSNLDILMMIGECLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      QWDLTLEDEREVITAITVILGSVANKELQNKLLTQLLSSSYGVLSKLVDEDAESSGRQ
SPATYTRMLSSVTRGLYRIGTVFSHLATSLPSVPADGPILSLLTVFWPILEKLFRSE
HMESGSLAAAACRALSVAVQSSGEHFWLLLPSVLDCLSRNFLSFQSQECYIRTACVIA
Chan, M.M., Chang, C.H., Dale, J.M., Hayashizaki, Y., Hsuan, V.W.,
Ishida, J., Jones, T., Kamiya, A., Karlin-Neumann, G., Kawai, J.,
Lam, B., Lee, J.M., Lin, J., Miranda, M., Narusaka, M., Nguyen, M.,
Onodera, C.S., Palm, C.J., Quach, H.L., Sakurai, T., Satou, M., Seki, M.,
Southwick, A., Tang, C.C., Toriumi, M., Wong, C., Wu, H.C., Yamada, K.,
Yu, G., Yuan, S., Shinozaki, K., Davis, R.W., Theologis, A. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EEPCHKEEYGSLF1TTFERFTQASSLMGINSSYICDQEPDLVEATVNFASALIRSCHK
ELGTGSGTLLEISFIKAAICCTAMIHGAALAAMSYLSGFLEVSLSSMIFTYNSI 3DGS
FSVVSVQVVSHCGEGLLSNTALLGVAAMSRVHKCGTILQQUAT
LCWKSLQGWINSAVMALPSEYIKQGERSIIVREWSBALGGAGIDYLENKSCNFGSNNS
                                                                                                                                                                                                                                                                                                                 Submitted (23-DEC-2002) Salk Institute Genomic Analysis Laboratory (SIGNAL), Plant Biology Laboratory, The Salk Institute for Biological Studies, 10010 N. Torrey Pines Road, La Jolla, CA 92037,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Cheuk, R. (SSP/Salk) and Seki, M. (RIKEN GSC) contributed equally to this work. Shinozaki, K. (RIKEN GSC) and Ecker, J.R. (SSP/Salk) contributed equally to this work as PIs.

Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The Salk, Stanford, PGEC (SSP) Consortium members constructed and sequenced the pUNI (ORF) clones using the RAFL cDNAs: Cheuk,R., Chen,H., Kim,C.J., Shinn,P., Bowser,L., Chan, M.M., Chang,C.M., Bale,J.M., Hsuan,V.W., Jones,T., Karlin-Neumann,G., Lam,B., Lee,J.M., Lin,J., Miranda,M., Nguyen,M., Onodera, C.S., Palm,C.J., Quach,H.L., Southwick,A., Tang,C.C., Toriumi,M., Wong,C., Wu,H.C., Yamada,K., Yu,G., Yuan,S., Davis,R.W., Theologis,A., and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       collection and clustering of RAFL CDNAS (RAFL CDNA: 'RIKEN Arbidopsis Full-Length CDNA'): Seki,M., Narusaka,M., Ishida,J., Sacou,M., Kamiya,A., Sakurai,T., Carninci,P., Kawai,J., Hayashizaki,Y. and Shinozaki,K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RIKEN Genomic Sciences Center (GSC) members carried out
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 3018;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2484 AGCTGCAATGTCATACTTATCAGGTTTCTTGGAGGT 2519
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SGGHMQGKHGRTLKRLVRDFADSHRNDPNPNI I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 23.2; DB 15;
Pred. No. 2.3e+02;
0; Mismatches 8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3 AGCTGCTTGGTCAGACTTATCCAGATTCTTGGCGGT 38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 organism="Arabidopsis thaliana"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            'ecotype="Columbia"
'note="This clone is in pUNI 51"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               'note="unknown protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /mol_type="mRNA"
/db xref="taxon:3702"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        chromosome="1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                clone="U13172"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      'codon start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 58.0%;
Best Local Similarity 77.8%;
Matches 28; Conservative
                                                                                                                                                                                                                                                                                 Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   i. .3018
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ecker, J.R.
                                                                                                                                                                                                                                                                                                                                                                                                                                    USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bource
                                                                                                                                                                                                                                                                             TITLE
JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ORIGIN
```

```
RESULT 9
CR380948 3
WPCOMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 10
AC099319/c
LOCUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOURCE
ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                             3'UTR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    VERSION
KEYWORDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REPERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                    ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ð
                                                                                                                                                                                                                                           Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnollophyta; eudicotyledons; core eudicotyledons; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

1 (Dases 1 to 3292)

2 Shinn, P., Chen, H., Cheuk, R., Kim, C.J., Koesema, E., Meyers, M.C., Hayashizaki, Y., Ishida, J., Jiang, P. X., Jones, T., Kanlih, A.D., Hayashizaki, Y., Ishida, J., Jiang, P. X., Jones, T., Kanlih, A.D., Miranda, M., Narusaka, M., Nguyen, M., Condera, C.S., Palm, C.J., Miranda, M., Narusaka, M., Nguyen, M., Onodera, C.S., Palm, C.J., Tang, C.C., Toriumi, M., Yamada, K., Yamamura, Y., Yu, G., Yu, S., Shinozaki, K., Davis, R.W., Theologis, A. and Bcker, J.R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note="unknown protein"
/codon start=1
/product="At1g12930/F13K23_14"
/protein id="AAK9148.1"
/db_xref="G1:1215746"
/translation="MELQRKVARAIHVLANHDPESSNRVAANQMLVQFQLTPAAMDVST
SLLTSPIVSLFDLQFFAAQILERKIQNBASNLQSTAKDALLNALLLAAKRYSSGVPQL
                                  Aruso402
Arabidopsis thaliana At1g12930/F13K23_14 mRNA, complete cds.
AY050402
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Shinn, P., Chen, H., Cheuk, R., Kim, C.J., Koesema, E., Meyers, M.C., Shinn, P., Chen, H., Cheuk, R., Kim, C.J., Koesema, E., Meyers, M.C., Banh, J., Bowser, L., Carninci, P., Dale, J.M., Goldsmith, A.D., Hayashizaki, Y., Ishida, J., Jiang, P.X., Jones, T., Kamiya, A., Miranda, M., Narusaka, M., Nguyen, M., Lee, J.M., Lin, J., Liu, S.X., Pham, P.K., Quach, H.L., Sakural, T., Satou, M., Seki, M., Southwick, A., Tang, C.C., Toriumi, M., Yamada, K., Yamamura, Y., Yu, G., Yu, S., Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The Salk, Stanford, PGEC (SSP) Consortium members carried out the sequencing and annotation of the RAFL CDNAs: Shinn, P., Chen, H., Cheuk, R., Kim, C.J., Koesema, E., Meyers, M.C., Banh, J. Bowser, L., Lan, J., Goldsmith, A.D., Jiang, P. X., Jones, T., Karlin-Neumann, G., Dane, J. Lee, J.M., Lin, J., Liu, S.X., Miranda, M., Nguyen, M., Ondekar, C.S., Palm, C.J., Pham, P.K., Quach, H.L., Southwick, A., Tang, C.C., Toriumi, M., Yamada, K., Yamamura, Y., Yu, G., Yu, S., Pavis, R.W., Theologis, A., and Ecker, J.R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted (16-UUL-2001) Salk Institute Genomic Analysis Laboratory (SIGNAL), Plant Biology Laboratory, The Salk Institute for Biological Studies, 10010 N. Torrey Pines Road, La Jolla, CA 92037,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Shinn, P. (SSP/Salk) and Seki, M. (RIKEN GSC) contributed equally to this work. Shinozaki, K. (RIKEN GSC) and Ecker, J.R. (SSP/Salk) contributed equally to this work as PIs. Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RIKEN Genomic Sciences Center (GSC) members carried out the collection and clustering of RAFL cDNAs (RAFL cDNA; 'RIKEN arbidopsis Full-Length cDNA'): Seki,M., Narusaka,M., Ishida,J., Satou,M., Kamiya,A., Sakurai,T., Carninci,P., Kawai,J., Hayashizaki,Y. and Shinozaki,K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   organism="Arabidopsis thaliana"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /clone="RAFL08-08-118(R13172)"
                                                                                                                                                                                          Arabidopsis thaliana (thale cress)
Arabidopsis thaliana
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /mol_type="mRNA"
/db_xref="taxon:3702"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /ecotype="Columbia"
1. .79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       chromosome="1"
                                                                                                                                        AY050402.1 GI:15215745
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      80. 3097
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1. .3292
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Unpublished
                                                                                                                                                                     CDNA.
                                                                           DEFINITION
ACCESSION
VERSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bource
                                                                                                                                                                KEYWORDS
SOURCE
ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         5'UTR
CDS
                                                                                                                                                                                                                                                                                                                                      REFERENCE
AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REFERENCE
AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE
JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TITLE
RESULT 8
AY050402
LOCUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMMENT
```

```
from base 300001 (CR380948 Candida glabrata strain CBS1
FSHHSDLRQELISHTSWYLDFILQQSENQFVSFLYPHDNNRKILRCLLSWYRAGCFSE
TPQGAVPSHPLLAYVENALQCTFPDLAIEVLYFRHBDLPQVLLYKRQFLADTLLK
PALINADLKI ISGLACLMSTEGQAAPCLI VERSSEALILTDAILSCVTFPSEDWEIAD
STVQFWSTFTY ISGLACKRQNDRTRYKDTFLPVFSALIVDALVLRAQVDEFTSSDES
GLDLPDGLLHFRNNLLELLVDICQLLHPTTFVSKLFPGGVPSSSVSMPLREIEAKLFA
LTAVSRIILOGGERAPPFALIMOLVSAFSVRESSELKGFISVYKSLADVVGSYSRNIS
OWDLTLEDBERTYTTVILGSVANKELQNKLHTQLLSSSVGVLSKLVDDILMNIGECLE
OWDLTLEDBERTYTTVILGSVANKELQNKLHTQLLSSSVGVLSKLVDEDBARSSGRQ
SPATYTRALSSVYTRGLYRIGTVFSHLATSLPSVPADGPILSLLTVFWPILEKLFRSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Akhter, N. Antonellis, A., Ayele, K., Beckstrom-Sternberg, S.M., Akhter, N., Antonellis, A., Ayele, K., Beckstrom-Sternberg, S.M., Benjamin, B., Blakesley, R.W., Bouffard, G.G., Breen, K., Brinkley, C., Brooks, S., Dietrich, N.L., Granite, S., Guan, X., Gupta, J., Haghighi, P., Hansen, N., Ho, S.-L., Idol, J.R., Karlins, E., Laric, P., Lee-Lin, S.-C., Legaspi, R., Maduro, Q.L., Maduro, V.B., Margulies, E.H., Masiello, C., Maskeri, B., Mastrian, S.D., Portnow, S.D., Promas, J.W., Portnow, M.C., Stantipopo, S., Thomas, J.W., Thomas, P.J., Touchman, J.W., Tsurgeon, C., Vogt, J.L., Walker, M.A., Wetherby, K.D., Wiggins, L., Young, A., Zhang, L.-H., and Green, E.D.
                                                                                                                                                                                                                                                                                                       HMESGSIAAAACRALSVAVQSSGEHFMILLPSVIDCISRNFISFQSQECYIRTACVIA
BEPCHKEBYSOSEPITTPERFTQASSIAGINSSYICDQEPDIABAYVBASALIRSCHK
BLLGTSGTLLEISFHKAAICCTAMHFRAALAMSYLEGFLEVSLSSMIETVNSISDGS
FSVVSVQVVSHCGGELLSNIVYALLGVAAMSKVHKCSTILQQLAAICSLCERTSWKGM
                                                                                                                                                                                                                                                                                                                                                                                                                                LCWKSLOGWINSAWALPBBYLKQGBAESYYRWSWSBALGGAGIDYLENKSCNFGSNNS
SGGHMQGKHGKTLKRLVRDFADSHRNDPNPNII"
3098. .3292
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AC099319 157285 bp DNA linear HTG 30-MAY-2002
Felis catus clone RP86-552N9, WORKING DRAFT SEQUENCE, 7 ordered
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Laurasiatheria, Carnivora, Fissipedia, Felidae,
Felinae, Felis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 58.0%; Score 23.2; DB 15; Length 110000; Best Local Similarity 77.8%; Pred. No. 1.5e+02; Matches 28; Conservative 0; Mismatches 8; Indels 0; 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LOCUS CR380948 Accession CR380948
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 3292;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indele
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            25537 CTGGATGTTGTAACTTATCTAGATTCTTTGCGGTAG 25572
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2563 AGCIGCAATGICATACTIAICAGITICITIGAAGI 2598
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 23.2; DB 15;
Pred. No. 2.3e+02;
0; Mismatches 8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3 AGCTGCTTGGTCAGACTTATCCAGATTCTTGGCGGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 5 CTGCTTGGTCAGACTTATCCAGATTCTTGGCGGTAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 110000
210000
310000
410000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AC099319.2 GI:21263264
HTG; HTGS PHASE2; HTGS_DRAFT.
FElis catus (cat)
Felis catus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Fragment Name Begin Br

(R280948 0 100001 21

CR380948 2 200001 31

CR380948 3 300001 41

CR380948 4 400001 50

CR380948 6 5 of CR380948 fr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence split into 5 fragments
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 58.0%;
Best Local Similarity 77.8%;
Matches 28; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AC099319
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        pieces.
```

```
Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     44654 AGAGCTGCTACTTCAGACTTCACTAGGTTCTTGGAG 44619
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 58.0%; Score 23.2; DB 14; Best Local Similarity 77.8%; Pred. No. 1.4e+02; Matches 28; Conservative 0; Mismatches 8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 AGAGCTGCTTGGTCAGACTTATCCAGATTCTTGGCG 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /estimated length=unknown 36308. 95535 /note="assembly_fragment" 88773. 157285 /note="clone overlaps with Ge AC099318 clone RP86-552L21 (c) 95536. 95635
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /estimated length=unknown 95636. 115087 /note="assembly_fragment" | 115088. 115187 /estimated length=unknown 115188. 154461
                                                                                                                                                                                                                                                                                                                                                                              /estimated length=unknown
13218. 21505
/note="assembly_fragment"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /estimated length=unknown 21606. 36207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              'note="assembly_fragment"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      154462. .154561 /
/estimated_length=unknown
                                                                                                                                                                                     1. .13117
/note="assembly_fragment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       'note="assembly_fragment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    vector_side:right"
                                                                                                                                                                                                                                                                                                     vector_side:left"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AC113932.2 GI:23396280
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Hominidae; Homo.
1 (bases 1 to 194645)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               clone_end:SP6
                                                                                                                                                                                                                                                                         clone_end:T7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens (human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Direct Submission
Unpublished
                                            /clone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Haugen, B.D.
                                                                                misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                  misc_feature
                                                                                                                                                                                         misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 11
AC113932/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REFERENCE
AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TITLE
JOURNAL
REFERENCE
AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE
JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       gap
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      gap
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   VERSION
KEYWORDS
                                                                                                                                                                                                                                                                                                                                                          gap
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              gap
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             gap
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               gap
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The sequence data in this record represents an 'enhanced' version of a Phase 2 submission. Specifically, the indicated order and orientation of each sequence contigl has been established using one or more of the following: read-pair data from individual subclones, overlaps with neighboring clones, alignment with available reference sequence (e.g., human), and/or confirmation by PCR testing. In addition, the sequence assembly is based on at least 8% average coverage in Q20 bases and has been reviewed to rule out gross misassemblies, the low-quality ends of sequence contigs have been trimmed away, and each base is associated with a Phrap-derived quality score.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         **NOTE: This is a 'working draft' sequence. It currently consists of 7 contigs. Gaps between the contigs are represented as runs of N. The order of the pieces is believed to be correct as given, however the sizes of the gaps between them are based on estimates that have provided by the submittor.

**This sequence will be replaced by the finished sequence as soon as it is available and the accession number will be preserved.

**13117: contig of 13117 bp in length 13217: contig of 13117 bp in length 13217: contig of 8288 bp in length 21505: contig of 14602 bp in length 36208: 36307: gap of unknown length 36208: 36307: gap of unknown length 36208: 36307: gap of unknown length 36308: 95535: contig of 19452 bp in length 36308: 115187: gap of unknown length 36308: gap of unknown
                                                                                                                                                    Direct Submission
Submitted (09-NOV-2001) NIH Intramural Sequencing Center, 8717
Grovemont Circle, Gaithersburg, MD 20877, USA
3 (bases 1 to 157285)
                                                                                                                                                                                                                                                                                                                                                                                  Submitted (30-MAY-2002) NIH Intramural Sequencing Center, 8717 Grovemont Circle, Gaithersburg, MD 20877, USA On May 30, 2002 this sequence version replaced gi:16874852.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequencing vendenty controlled in the controlled
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      contig of 39274 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              gap of unknown length contig of 2724 bp in length.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Center: NIH Intramural Sequencing Center
Center code: NISC
Web site: http://www.nisc.nih.gov
Contact: nisc zoo@nbgri.nih.gov
NISC Comparative Sequencing Initiative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /organism="Felia catus"
/mol type="genomic DNA"
/db xref="taxon:9685"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Center project name: cuh
Center clone name: 552N09
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers
                                            Unpublished
2 (bases 1 to 157285)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  154561:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          157285:
                                                                                                                                                                                                                                                                                                                                                     Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          115188
154462
154562
                                                                                                                    Green, E.D.
                                                                                                                                                                                                                                                                                                             Green, B.D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bource
                                                                            REFERENCE
AUTHORS
                                                                                                                                                        TITLE
JOURNAL
                                                                                                                                                                                                                                                                 REFERENCE
AUTHORS
TITLE
JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMMENT
```

```
ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRI 01-OCT-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Zer (bases 1 to 194645)
Kaul,R.K., Olson,M.V., Raymond,C. and Haugen,B.D.
Direct Submission
Submitted (05-MAR-2002) Genome Center, University of Washington,
Box 352145, Seattle, WA 98195, USA
3 (bases 1 to 194645)
1. .22574
/note="clone overlaps with GenBank Accession Number
AC099317 clone RP86-503B21 (center project name cug)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GenBank Accession Number (center project name cui)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AC113932 194645 bp DNA linear PRI 01-OCT
Homo saplens chromosome 3 clone RP11-757H2, complete sequence.
AC113932
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Kaul,R.K., Olson,M.V., Zhou,Y., James,R.A., Rouse,G., Wu,Z.,
Saenphimmachak,C., Buckley,D., Kibukawa,M., Raymond,C. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 157285;
```

seq3-then-seq4.rge

653	н	1757	8104	4786	<800	<800	3727	6251	3855	6489		1515	14394	×800	6489	1389	1515	10366	<800	2759	5367	5367	1515	<800	2759	4089	953	6439	<800	5562	5367	×800			
F2F1	1296	1762	8246	4727	199	592	3698	6206	3901	6476	1003	1544	14199		6235	1415	1579	10496	225	2734	5415	5415	1511	425	2671	4101	893	6764	643	5525	5333	571	2573	6824	
0742	4847	857	<800	2490	2752	771	<800	6221	10255	8742	21093	<800	2752	1209	7054	3151	<800	9194	9761	5065	7940	2490	15084	9761	<800	<800	2752	4327	<800	1209	4055	15084	5065	! !	
1 1 0	4881	853	82	2437	2566	771	338	6143	10330	8577	20801	533	2749	1251	7011	3029	209	9188	9864	5084	7869	2358	15440	9764	118	643	2723	4369	475	1227	4025	15077	4985	1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	
2750	883	2428	7313	<800	2428	3254	725	26263	2650	2892	10948	4171	3516	7877	4171	1807	6867	5684	1049	1674	<800	1251	5921	4171	<800	1251	<800	15569	3516	4171	1251	816	1674	3363	0000
7767	882	2297	7254	309	2403	3079	721	25979	2457	2735	11178	4127	3491	7816	4231	1832	6822	5708	1047	1710	63	1232	5849	4169	224	1249	282	15810	3477	4043	1298	818	1704	3246	0 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7
ıd, C. and	Direct Submission Submitted (01-OCT-2002) Genome Center, University of Washington,	.9111737.	to					8)			ntigs		bp overlap			ality zero. s than	ible from the	!	This sequence was finished as follows unless otherwise noted:	ed with an a (i.e., Phred	<pre>quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were</pre>	than one M13 ction digest.		olete Digest derived digest	both insert and	re circular BAC. ately 400-800 bp)	are not resolved in the ringerprint and hence do not appear in the table. There are no significant remaining discrepancies	iiqueiy oraerea	HINGLII	:Map FngrPrnt		1073 1042	6382 6489	512 <800	440
M., Raymon	niversity	laced gi:1	ome Center	on.edu		1)	reads	reads 5% of reads	90319 east Q40	east Q30 east Q20	eum-of-co		6 92, 86357-	,	ence quall y program.	uced to qu have less	erally vis	bie as par	less other	or sequenc uality dat	esolve all ts; all re	or more t		tiple Comp imentally	ents 18 g1 nsists of	r the enti (approxim	remaining	values. on		t SeqDerMap			į		
thak, C., Buckley, D., Kibukawa, M., Raymond, C.	ne Center, U	Box 352145, Seattle, WA 98195, USA On Oct 1, 2002 this sequence version replaced gi:19111737	Center: University of Washington Genome Center Center: University of Washington Genome Center	Center Code: once Web Bite: http://www.genome.washington.edu Contact: www.ptge@n washington edu	nation	Center clone name: CIII-3 Center clone name: RP11 (bc0771)	d; 100% of	Big Dye; 4	version 0.9 bases at 1	bases at l	Insert sizē: 194645; sum-of-contigs Quality coverage: 7.5x in Q20 bases; sum-of-contigs		5': RP11-41F5 (UWGC:bc0157) AC020626 3': RP11-668D4 (UWGC:bc0770) AC116992, 86357-bp overlap	equence Quality Assessment:	a witn sequ irap assembl	ive been red expected to	l error in 10,000 bp. Base-by-base quality values are not generally visible f	are avalla	follows un	e-stranded d by high q	is made to r is and repea	nid subclone us confirmed		lated by Mul of the exper	ncted rragm sequence co	able cutoff	Jerprint and Jignificant	predicted lashed lines	BCOKI	lap FngrPrnt		8696 8742	6 <800	559 <800	1000
Buckley, D.	002) Genom	Box 352145, Seattle, WA 98195, On Oct 1, 2002 this sequence v	ity of Was	//www.genc	ect Inform	me: RP11-7	or: plasmi	terminator terminator	m: Phrap; ty: 194343	ty: 194638 ty: 194645	4645; sum- e: 7.5x in	 0	(UWGC:bc01 (UWGC:bc0	sessment:	n annotate by the Ph	d bases ha ve 40 are	bp. ty values	N.1 file.	inished as	ther doubl	attempt wa ompression	one plasm ssembly wa		been valid mparison o	uence-prec -digested	o accurate low a vari	n the ring e are no s	mental and rated by d		SeqDerMap		869			
Saenphimmachak, C., E	mission (01-OCT-20	, Seattle 2002 this	: Univers	te: http:/	Proje	clone nar	cing vect	try: Dye- try: Dye-1	ly program sus qualit	sus qualit	Insert sizė: 19464 Quality coverage:	g Sequence	P11-41F5 P11-668D4	uality ABE	y nas been computed	lly editer evels abor	n 10,000 J ase qualit	ntry's AS	nce was fi	s were ei chemistry	30); an e such as co	at least and the as	equence Validation:	ence has l nting. Com	with sequentiality.	n order to gments bel	ble. There	are sepan		FngrPrnt		13311	2045	9318	9
imma G	Direct Submission Submitted (01-OCT	x 352145 Oct 1,	Center	Web si	1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	Center	Sequen	Chemis	Assemb	Consen	Insert	verlappin	3,:	Sequence O	Thib entrestimates	All manua Quality	l error 1 Base-by-b	Genbank r of this e	his seque	111 region 11ternate	<pre>pality >= roblems, and an arrangement</pre>	covered by subclone;	Sequence Va	This sequ fingerpri	rragments The elect	Small fra	are not r in the ta	fragments	169	SeqDerMap		13641	2067	9264	
Saenph	Sub	8 6	:		•							' 0		ı Ø					н	10 10	O. 174	U W							•		•	'	'	,	

REFERENCE 2 (bases 1 to 201467) AUTHORS Worley, K.C. TITLE Direct Submission JOURNAL Submitted (30-MAR-2000) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA REFERENCE MOLECLEY, K.C. TITLE Submitted (01-DEC-2000) Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA REFERENCE MOLECULAR and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA REFERENCE MOLEY, K.C. TITLE JOURNAL OF NOTEY, K.C. TITLE JOURNAL OF NOTEY, K.C. MOLECULAR and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA AUTHORS Worley, K.C. TITLE JOURNAL OF NOTEY, K.C. TITLE JOURNAL JOURNAL OF NOTEY, K.C. TITLE JOURNAL JOURNAL OF NOTEY, K.C. TITLE JOURNAL OF NOTEY, K.C. TITLE JOURNAL JOUR	Adrian Smit. Sequence similarities were identified using Powerblast by Jinghui Zhang. Exon/Intron boundaries of identified genes were chosen if there were canonical splice junctions that maintained sequence continuity	4		repeat_region
5705 5814 1360 1389 1360 1389 755 <800 2612 2759 2612 2759 7611 5562 7840 4786 78589 5562 7870 5814 7870 5814 7870 6814	tens" DNA"	Score 23.2; DB 8; Length 194645; Pred. No. 1.46+02; O; Mismatches 8; Indels 0; Gaps 0; TCCAGATTCTTGGCGT 38 TCCACATTATACCTGT 157156	AC027298 201467 bp DNA linear ROD 05-DEC-2000 Mus musculus 7 BAC RP23-266F22 (Roswell Park Cancer Institute Mouse BAC Library) complete sequence. AC027298 AC027298.20 GI:11496331 Mus musculus (house mouse) Mus musculus (house mouse) Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Butheria; Buarchontoglires; Glires; Rodentia; Sciurognathi; Muroidea; Murinae; Mus.	1 bases 1 to 201467) Semetzker,M.L., Lewis,L.R., Hume,J., Edwards,C., Harris,C., Dederich,D., Thomas,S., Okwuonu,G., Carlock,C., Garner,T., Addison,S., Pace,A., Williams,G., Bonnin,D., Brooks,A., Brown,J., Buhay,C., Bunac,C., Darkett,C., Chacko,J., Chen,G., Chen,Z., Cox,C., Davis,C., DingyY., Dugan-Rochs,S., Fernandez,C., Ferraguto,D., Forcum-Tansey,J., Gill,R., Gorrell,J.H., Gunaratne,P., Haller,G., Hernandez,J., Hogues,M., Hosak,H., Hou,X., Huber,J., Jackson,L., Jia,Y., Kelly,J., Kelly,S., Kovar,C., Liu,J., Liu,W., Loulseged,H., Lozado,R.J., Martin,R., Massey,B., McLeod,M.P., Mei,G., Moore,S., Morgan,M., Martin,S., Perez,L., Reiter,D., Say,J., Shen,H., Vasquez,L., Watlington,S., Williamson,A., Wrensford,G., Zhou,X., Bouck,J., Hodgson,A., Wazny,D.M., Rives,M., Scherer,S., Sodergren,B., Weinstock,G., Direct Submission
1621 1674 1621 1674 3355 3393 4209 4171 1174 1146 4721 4656 1957 1912 3929 3907 2661 2758 1751 1674	cation/Qua .194645 .ganism="H ol_type="G _xref="ta	Cuery Match 58.0%; Score 23.2; DB 8; Len Best Local Similarity 77.8%; Pred. No. 1.46+02; Matches 28; Conservative 0; Mismatches 8; In Qy 3 AGCTGCTTGATCAGATTATCCAGATTTTGGGG 38 Db 157191 AGCAGCTTGGTCTGAATTATCCACATTATACCTGT 157156 RESULT 12	AC027298 LOCUS AC027298 LOCUS AC027298 AC027298 ACCESSION AC027298	REFERENCE 1 (bases 1 to 201467) AUTHORS Metzker,M.L., Lewis,L.R., HU Dederich,D., Thomas,S., Okwa Addison,S., Pace,A., William Buhay,C., Bunac,C., Burkett, Cox,C., Davis,C., Delgado,O., Fernandez,C., Ferraguto,D., Gorrell,J.H., Gunarathe,P., HOBAK,H., HOU,X., HUDE,T.J., KOVAT,C., Liu,J., Liu,W., LC, Massey,E., McLeod,M.P., Mei, Neal,D., Nelson,A., Nguyen,F Perez,L., Reiter,D., Say,J., Milliamson,A., Wrensford,G., Milliamson,A., Wrensford,G., Worley,K. and Gibbs,R.

```
Query Match 58.0%; Score 23.2; DB 9; Length 201467; Best Local Similarity 77.8%; Pred. No. 1.46+02; Matches 28; Conservative 0; Mismatches 8; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                115057 CTTCTTGGTGACACATAGGAAGATTCTTGGGGGTAG 115092
                                                                                                                                                                                                                                                                                                                                                                                                                                                  5 CTGCTTGGTCAGACTTATCCAGATTCTTGGCGGTAG 40
                                      /rpt_family="RMBR20"
65340. 65510
/rpt_family="LKB"
complement (65954. 66079)
/rpt_family="RMBR20"
66080. 66418
/rpt_family="LKS"
66419. 66458
/rpt_family="LKS"
66459. 66131
/rpt_family="LKS"
66899. 67131
/rpt_family="LKS"
67148. 67201
/rpt_family="LKS"
67149. 67301
/rpt_family="LKS"
67149. 67301
 complement (60438. .62610)
             /rpt_family="Lx2"
65129. .65223
                                                                                                                                                                                                                                                                                                                                           /rpt_fami_,
68188. .68440
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AC116992.2 GI:21306689
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens (human)
Homo sapiens
 repeat_region
                                                                                                                                                                                                                                                                                                                             repeat_region
                                                                                                                                                                                                                                                                                                                                                              repeat_region
                              repeat_region
                                                            repeat_region
                                                                                       repeat_region
                                                                                                                     repeat_region
                                                                                                                                                    repeat_region
                                                                                                                                                                               repeat_region
                                                                                                                                                                                                             repeat_region
                                                                                                                                                                                                                                           repeat_region
                                                                                                                                                                                                                                                                       repeat_region
                                                                                                                                                                                                                                                                                                   repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                VERSION
KEYWORDS
SOURCE
ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 13
AC116992
LOCUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REFERENCE
AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TITLE
JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REFERENCE
AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TITLE
JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                  ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note="Region similar to Mm#S176249 vb56h02.rl Mus musculus cDNA; gb=AA387402"
complement (35348. .35455)
/rpt family="ETHERV2"
                                                                                                                                                                                                                                 /rpt family="ThERV2"
complement (31847. .32382)
/rpt family="Warrn"
complement (3730.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /rpt_family=
36378. 36460
/rpt_family="A-rich"
complement(36461. 36757)
/rpt_family="Lx7"
                                                                                                                                                                                                                                                                                                                                                                                      33403. .33884
/rpt_family="LTRIS_NM"
complement (33885. .33949)
/rpt_family="ETHEKP2"
complement (33997. .34265)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        41777. .41917

/rpt_family="L1"

/rpt_family="L4". .42321)

/rpt_family="Lx2"

/rpt_family="Lx2"

/rpt_family="Lx2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     58666. .58786
/rpt_family="HERVL"
59692. .60261
/rpt_family="MT-INTERNAL"
60314. .60343
/rpt_family="(TTTA)n"
                                                                                                                                                                                                                                                                                                                                                                                                                                           family="ETDERV2"
ement(3457
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   rpt_family="LIVL2"
:8666. .58706
                                                     22308. .22337
/rpt_family="(TTTG)n"
complement (24534. .24625)
/rpt_family="11"
               /rpt_family="Lx4"
complement(21486. .22307)
/rpt_family="Lx4"
                                                                                                                                                                                                                                                                                                complement (32387. .33027) /rpt_family="ETnERV2"
                                                                                                                                                                                                                                                                                                                             complement (33013. .33334) /rpt_family="ETnERV2"
complement (20835. .21490)
                                                                                                                  complement (24623. .24743)
/rpt_family="L1"
                                                                                                                                                                                                                                                                                                                                                         omplement (33349. .33402) rpt family="BTnERV2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         complement (36850. .38900)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      complement (38914. .40129) /rpt_family="Lx2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     complement (40132. .40249)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   rpt_family="L1_MM"
6292. .36343
rpt_family="(CATATA)n"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  family="RLTR13D"
                                                                                                                                                                               . .26259
family="RLTR10"
                                                                                                                                                              family="L1 MM"
                                                                                                                                                                                                          9<u>240</u>. .29697
rpt_family="L1 MM"
omplement(30087. .3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            54195. .54661
/rpt family="L1 MM"
complement (56789. .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 40592. .41250
/rpt_family="L1"
41396. .41541
/rpt_family="L1"
repeat_region
                                                                                                                                                                                                                                                                    repeat_region
                             repeat_region
                                                          repeat_region
                                                                                      repeat_region
                                                                                                                     repeat_region
                                                                                                                                                repeat_region
                                                                                                                                                                              repeat_region
                                                                                                                                                                                                           repeat_region
                                                                                                                                                                                                                                        repeat_region
                                                                                                                                                                                                                                                                                                   repeat_region
                                                                                                                                                                                                                                                                                                                                repeat_region
                                                                                                                                                                                                                                                                                                                                                            repeat_region
                                                                                                                                                                                                                                                                                                                                                                                        repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                     repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                  repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              misc_feature
```

ô

Gaps

```
PRI 01-JUN-2002
                                                                                                                                                                                                                                                                                                                                    and Haugen, E.D.
Direct Submission
Uppublished
2 (bases 1 to 204162)
Kaul, R.K., Olson, M.V., Raymond, C. and Haugen, E.D.
Direct Submission
Direct Submission
Box 352145, Seattle, WA 98195, USA
3 (bases 1 to 204162)
3 (bases 1 to 204162)
Samphimmachak, C., Phelps, K.A., Buckley, D., Kibukawa, M., Raymond, C.
                                                                                                                                                                                                                                        Hominidae, Homo.
I (bases 1 to 204162)
Kaul, R.K., Olson, M.V., Zhou, Y., James, R.A., Rouse, G., Wu, Z.,
Saenphimmachak, C., Phelps, K.A., Buckley, D., Kibukawa, M., Raymond, C.
                                                                                                                                                                                          Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ACI16992 204162 bp DNA linear PRI 01-JUJ
Homo sapiens chromosome 3 clone RP11-668D4, complete sequence.
AC116992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Web site: http://www.genome.washington.edu
Contact: uwgchtgs@u.washington.edu
------ Project Information
Center project name: chr-3
```

<800 2206 <800 20634	7342 767 3402 1002	8802 <800 <800 10341 8802	8802 4849 862 800	2458 2627 <800 <800 6210 10341	20634
2233	1 1 1	8656 467 467 559 10575 8632	883 883 883 883	2437 2566 771 338 6143 10330	2001
2701 5381 10288 <800	1594 1096 4800	1015 1397 3050 2347 2880	2701 <800 <800 6828	2181 922 6 800 4300 6800 1397	3400 4300 2347 1096 6800 1397 6800 4300 14463 2042 6800
2771 5512 10558 449	16679	1017 1415 3045 2201 2809	2625 2625 95 570 6870	2136 925 925 783 4405 556 556	13391 4252 2386 1095 179 627 627 677 677 14905 2006 31
2927 1551 2101 9842	7283 4152 1317 1876	6711 6229 3858 959 4152	1876 1551 5568 959	6711 10472 3488 3219 2101 5350 <800	2927 2759 876 2400 7283 <800 2400 3219 722 26167 2615 2927
2952 1596 2092 10117	1 1 1	6673 6255 3953 4 964 4308	1882 1605 5620 968	0809 10741 10741 3320 3320 2121 2121 5525 404	2654 2654 882 882 72297 7255 309 3079 3079 3079 2457 2457 2457
Center clone name: RP11-668D4 (bc0770)	ansus quality: Jostes at least Q20 tt size: 20462; sum-of-contigs tty coverage: 8.2x in Q20 bases; sum-of-contigs 	requence Quality Assessment: This entry has been annotated with sequence quality setimates computed by the Phrap assembly program. All manually edited bases have been reduced to quality zero. Quality levels above 40 are expected to have less than 1 error in 10,000 bp. Base-by-base quality values are not generally visible from the GenBank flat file format but are available as part of this entry's ASN 1 file.	This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., Phred quality, >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest.	e Complete tally derivable derivable for both complete on the	SeqDerMap FngrPrnt SeqDerMap FngrPrnt 21681 22111 8696 8802 1823 1842 6 6800 2912 2880 5030 5004 463 <800 5757 5717 2349 2347 12366 12038 5483 5381 14141 13920 5483 6800 8270 8215 21 <800 4241 4265 216 <800 4300 4265 216 <800 4300 4265

Rail Stain S	1 1	
TITLE JOURNAL REFERENCE TITLE JOURNAL	COMMENT	
REFEREN	Š	
4127 4152	/ Match Local Similarity 77.8%; Score 23.2; DB 8; Length 204162; Local Similarity 77.8%; Pred. No. 1.48+02; Les 28; Conservative 0; Mismatches 8; Indels 0; Gaps 0; 3 AGCTGCTTGGTCAGACTTATCCAGATTCTTGGCGT 38	AC165609 Bos taurus clone CH240-169M19, *** SEQUENCING IN PROGRESS ***, 25 unordered pleces. ON AC165609 AC165609 (G170012627) AC165609 (G170012627) AC165609 (G170012627) AC165609 (G170012627) Bos taurus (Cow) ISM Bos taurus (Cow) ISM Bos taurus (Cow) Bos taurus (Cow) IGEN Bovinae, Bovinae, Bos. ICE (Gases I to 82207) AC16500 (Gases I to 82207) ICE (Cases I to 82207) AC16600 (Gases I to 82207) AC16000
	Query M Best Lo Matches Qy Db 15	RESULT 14 ACLIGE 609/C LOCUS DEFINITION ACCESSION VERSION VERSYON SOURCE ORGANISM AUTHORS

```
Rabata,D., Rachlin,B., Reigh,R., Ren,Y., Reuter,M., Richards,S., Rives,C., Rodriguez,F., Rojas,A., Ruiz,S.J., Sana,M., Sanders,W., Santbanez,J., Santos,R., Savery,G., Scherer,S., Shen,H., Shen,Y., Sisson,I., Sneed,A., Sadesrer,S., Schelle,R., Svetek,A., Taylor,B., Taylor,T., Thomas,N., Thorn,R., Thornton,R., Trejos,Z., Usmani,K., Vargo,C., Verduzco,D., Villasana,D., Virk,D., Volkov,A., Waldron,L., Walker,B., Wang,C., Wang,S., Warren,J., Wei,X., Wheeler,D., Williams,G., Williams,R., Worley,K., Wright,R., Wu,J., Yakub,S., Yan,K., Yu,F., Zhang,J., Zhang,L., Zhou,J., Weinstock,G. and Gibbs,R. Direct Submission Unpublished
                                                                                                                                                                                                                                              NOTE: Bstimated insert size may differ from sequence length (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).
NOTE: This is a 'working draft' sequence. It currently consists of 25 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Quality coverage: 1x in Q20 bases; sum-of-contigs estimation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3112: gap of unknown length
3112: gap of unknown length
5319: contig of 2207 bp in length
5419: gap of unknown length
7498: contig of 2079 bp in length
7598: gap of unknown length
12514: contig of 4916 bp in length
12514: contig of 4916 bp in length
15270: contig of 2895 bp in length
15370: contig of 3995 bp in length
15365: contig of 3995 bp in length
15365: gap of unknown length
15365: contig of 2891 bp in length
22456: gap of unknown length
22456: gap of unknown length
22456: gap of unknown length
3138: contig of 5162 bp in length
31128: contig of 5162 bp in length
3125: contig of 5162 bp in length
31325: contig of 2427 bp in length
31325: contig of 2427 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        length
bp in length
length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               length
bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 gap of unknown 1
contig of 2790 b
gap of unknown 1
contig of 3504 b
gap of unknown 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          unknown
of 2259
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                unknown
of 2594
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                contig
gap of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              33725:
33825:
36615:
40219:
40319:
42578:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          31198:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3113
5320
5420
7499
7599
12515
12615
15271
15371
19366
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3013
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     22357
22457
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          25937
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                31299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       33826
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         36616
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            26037
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                31199
```

in length

contig

```
2: gap of unknown length
7: contrig of 3275 bp in length
6: gap of unknown length
6: gap of unknown length
7: contrig of 2847 bp in length
7: contrig of 2846 bp in length
7: contrig of 2115 bp in length
7: contrig of 4459 bp in length
7: gap of unknown length
7: gap of unknown length
7: gap of unknown length
7: contrig of 4351 bp in length
7: contrig of 4351 bp in length
7: contrig of 2522 bp in length
7: contrig of 2522 bp in length
7: contrig of 3222 bp in length
7: contrig of 4381 bp in length
7: gap of unknown length
7: contrig of 2566 bp in length
7: gap of unknown length
7: gap of unknown length
7: contrig of 2566 bp in length
7: contrig of 2567 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  42579. 42678 / 42579. 42579. 42579. 42573. 45272. 45272. 45272. 45872. 48648. 48747
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          69182. .69781
/estimated length=unknown
72504. .72603
/estimated length=unknown
76985. .77084
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /estimated_lengtn=unknown
25937. .26036
/estimated_length=unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /estimated length=unknown 33726. .33825 /estimated length=unknown 36616. .36715
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /estimated length=unknown
40220. 40319
/estimated_length=unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         51595. .51694
/estimated length=unknown
55335. .55434
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /estimated length=unknown 7499. .7598
/estimated_length=unknown 12515. .12614
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /estimated length=unknown 62109. .62208
                                                                                                                                                                                                                                                                                                                                                                                                                                                     /estimated_length=unknown
5320. .5419
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /estimated length=unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  19366. .19465
'estimated_length=unknown
22357. .22456
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     'estimated_length=unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               estimated length=unknown 17550. .57649
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             'estimated_length=unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    'estimated_length=unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                length=unknown
                                                                                                                                                                                                                                                                                                                                                                            /organism="Bos taurus"
/mol_type="genomic DNA"
/db_xref="taxon:9913"
                                                                                                                                                                                                                                                                                                                                                                                                                          /clone="CH240-169N19"
3013. .3112
                                                                                                                                                                                                                                                                                                                                             Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             31199. .31298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             56560. .66659
                                                                            55334:
55434:
57549:
57649:
                                                                                                                                                                                                                                                                                                               79750:
                                               51594:
                                                                                                                                                                                                                                                    72603:
                                                                                                                                                                                                                                                                 76984:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /estimated
                                                                51694:
   45273
463478
463478
46348
51695
51695
55335
55335
57650
62109
66560
66560
66560
66560
77698
77698
77085
                                                                                                                                                                                                                                                                                                                                                               source
                                                                                                                                                                                                                                                                                                                                               PEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                               gap
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              gap
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           gap
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        gap
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       gap
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    gap
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   gap
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                gap
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               gap
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              gap
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           gap
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          gap
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        gap
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       gap
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    gap
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     gap
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    gap
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    gap
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                gap
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                gap
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             gap
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              gap
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           gap
```

```
ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted (27-NOV-2003) Department of Genetics, Washington Submitted (27-NOV-2003) Department of Genetics, Washington University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA On Jul 30, 2003 this sequence version replaced gi:32490736.
                                                                                                                                                                                                                                                                                                                                                         AC130715 168935 bp DNA linear ROD 27-NOV-2003
Mus musculus BAC clone RP23-460116 from chromosome 2, complete
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequencing of Mus musculus
Unpublished (2001)
3 (bases 1 to 168935)
McPherson, J.D. and Waterston, R.H.
Direct Submission
Submitted (13-AUG-2002) Genome Sequencing Center, 4444 Forest Park
Parkway, St. Louis, MO 63108, USA
4 (bases 1 to 168935)
Wilson, R.K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       S Vosco. - --
Wilson,R.K.
Direct Submission
Submitted (30-JUL-2003) Genome Sequencing Center, 4444 Forest Park
Parkway, St. Louis, MO 63108, USA
6 (bases 1 to 168935)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Direct Submission
Submitted (10-701-2003) Genome Sequencing Center, 4444 Forest Park
Submitted (10-701-2003) MO 63108, USA
(Dases 1 to 168935)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NOTICE: This sequence may not represent the entire insert of this clone. It may be shorter because we only sequence overlapping clone sections once, or longer because we provide a small overlap between neighboring data submissions.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This sequence was finished as follows unless otherwise noted: all regions were double stranded, sequenced with an alternate chemistry, or covered by high quality data (1.e., phred quality >=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Butheria, Buarchontoglires, Glires, Rodentia,
Sclurognathi, Muroidea, Muridae, Murinae, Mus.
1 (bases 1 to 168936)
                                                                                                                                                         Gape
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Center: Washington University Genome Sequencing Center Center code: WUGSC Web site: http://genome.wustl.edu Contact: submissions@watson.wustl.edu
                                                                                                                                                         ö
                                                                                                          57.5%; Score 23; DB 14; Length 82207; 83.9%; Pred. No. 1.9e+02; ive 0; Mismatches 5; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Nguyen, C. and Kozlowicz, A.
The sequence of Mus musculus BAC clone RP23-460L16
Unpublished (2001)
2 (bases 1 to 168935)
                                                                                                                                                                                                                              25712 AGAGCTGCTTGTTCAGATTTGTCCAGAGCCT 25682
                                                                                                                                                                                                1 AGAGCTGCTTGGTCAGACTTATCCAGATTCT 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Center project name: M BA0460L16
/estimated_length=unknown
79651. .79750
/estimated_length=unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mus musculus (house mouse)
Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                        AC130715
AC130715.3 GI:33342436
HTG.
                                                                                                                               Local Similarity 83.9
hes 26; Conservative
                                                                                                            Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOURCE
                                                                                                                                                                                                                                                                                                                                                                              DEFINITION
                                                                                                                                                                                                                                                                                                             RESULT 15
AC130715
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REFERENCE
AUTHORS
JOURNAL
TITLE
JOURNAL
REFERENCE
AUTHORS
TITLE
JOURNAL
REFERENCE
AUTHORS
AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TITLE
JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REFERENCE
AUTHORS
TITLE
JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REFERENCE
AUTHORS
TITLE
JOURNAL
                                                                                                                                                         Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REFERENCE
AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                          ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                 VERSION
KEYWORDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMMENT
                                                                ORIGIN
                                                                                                                                                                                                                                            a
                                                                                                                                                                                                     ઠે
```

```
57.0%; Score 22.8; DB 9; Length 168935; 79.4%; Pred. No. 2.1e+02;
                                                                                                                                                                                                                                                                                                    /rpt_family="L1"
26493
/rpt_family="B4"
26744. .26902
/rpt_family="MER2_type"
26977. .27062
/rpt_family="MeR2_type"
27063 .27146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              'rpt_family="MER2_type"
                                                                                                            /rpt_family="BRVK"
21953. 22544
/rpt_family="RMER19B"
22545. .22666
/rpt_family="B4"
25044. .25656
                                                                                                                                                                                                                                                                                                                                                                                                                                                              rpt_family="RMBR6A"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /rpt_family="Malk"
41467. 41856
/rpt_family="L1"
42309. 42609
/rpt_family="L2"
43220. 43550
43568. 44665
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /rpt_family="ERV1"
31123. 31278
/rpt_family="B4"
31603. 31929
                                                                                                                                                                                                                                                                /rpt_family="Malk"
16056. .26348
                                                                               rpt family="ERVK"
.9588. .19966
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /rpt_family="MaLR"
44127. .44851
/rpt_family="MaLR"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           'rpt_family="MaLR"
.0284. .40336
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          rpt_family="MaLR"
0729. .40877
                 /rpt_family="L1"
18642. 19007
/rpt_family="L1"
19436. 19551
                                                                                                                                                                                                         /rpt_family="L1"
25655. .25729
/rpt_family="L1"
25730. .26055
                                                                                                                                                                                                                                                                                                                                                                                                                               'rpt_family="Alu"
17234. .27466
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /rpt_family="L1"
32844. .34072
/rpt_family="L1"
36213. .36494
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /rpt_family="Alu"
11335. .41461
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            rpt_family="B2"
9034. .29205
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         rpt_family="B4"
9476. .29555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            rpt_family="L1" | 19818. .39999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /rpt_family="B4"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              rpt_family="L1"
|9295. .39495
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               rpt_family="L1" 18832. .39288
                                                                                                                                                                                                                                                                                     .26348
    18217. .18571
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
    repeat_region
                                     repeat_region
                                                                                                                                                                                                                                                                                                                                                    repeat_region
                                                                  repeat_region
                                                                                                 repeat_region
                                                                                                                              repeat_region
                                                                                                                                                               repeat_region
                                                                                                                                                                                             repeat_region
                                                                                                                                                                                                                            repeat_region
                                                                                                                                                                                                                                                           repeat_region
                                                                                                                                                                                                                                                                                        repeat_region
                                                                                                                                                                                                                                                                                                                       repeat_region
                                                                                                                                                                                                                                                                                                                                                                                     repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                 repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                 repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                repeat_region
                                                                                            Mapping information for this clone was provided by Dr. Wes Warren, Department of Genetics, Washington University, St. Louis MO. For additional information about the map position of this sequence, see http://genome.wustl.edu
30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by sequence from more than one subclone; and the assembly was confirmed by
                                                                                                                                                                       SOURCE INFORMATION:

The RPCI-23 BAC Library has been constructed by Kazutoyo Osegawa and Minako Tateno in the laboratory of Pieter de Jong (http://www.chori.org) from female C57BL/6J mouse kidney and/or brain genomic DNA. The clone and detailed information can be obtained from Research Genetics, Inc. (http://www.resgen.com) or pieter de Jong and coworkers at http://www.corpi.org
                                                                                                                                                                                                                                                                                                 NEIGHBORING SEQUENCE INFORMATION:
This sequence is the entire insert of the clone. This clone is overlapped by AL928713 and AL929149.

Location/Qualifiers
1..168935
/organism="Mus musculus"
                                                                                                                                                                                                                                                                                                                                                                                               /mol_type="genomic DNA"
/db_xref="taxon:10090"
/chromosome="2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                           /clone="RP23-460L16"
/clone_llb="RPC1-23"
1. :56
/rpt_family="L1"
558...1161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /rpt_family="L2"
3626. 4150
/rpt_family="ERVL"
/rpt_family="ERVL"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /rpt_family="ERVK"
15597. .15702
/rpt_family="B4"
16614. .16767
/rpt_family="MalR"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /rpt_family="L1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /rpt_family="L1"
1249. .2023
/rpt_family="L1"
2589. .2727
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /rpt_family="B4"
6204_.6630
/rpt_family="L1"
8366_.8677
/rpt_family="L1"
8730_.9660
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    family="L1"
9. .13554
family="L2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              418. .4784
rpt_family="L1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         _family="L1" . 1251
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  rpt_family="L2"
4111. .14419
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       rpt family="L1"
2233. .12344
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               rpt_family="L1"
4422. .14699
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              family="L1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     .13794
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  .14419
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             .15651
                                                                               MAPPING INFORMATION:
                                                restriction digest
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      rpt_fa
3628.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            repeat_region
                                                                                                                                                                                                                                                                                                                                                                     source
                                                                                                                                                                                                                                                                                                                                                   FEATURES
```

ö

0; Gaps Matches 27; Conservative 0; Mismatches 7; Indels Search completed: April 18, 2006, 19:42:56 Job time : 954 secs දු ද

This Page Blank (uspto)

April 18, 2006, 19:05:32 ; Search time 219 Seconds (without alignments) 1217.295 Million cell updates/sec GenCore version 5.1.7 Copyright (c) 1993 - 2006 Biocceleration Ltd. nucleic search, using sw model OM nucleic Run on:

1 agagctgcttggtcagacttatccagattcttggcggtag 40 SEQ3-THEN-SEQ4 score: Title: Perfect sc Sequence:

IDENTITY NUC Gapop 10.0 , Gapext 0.1 Scoring table:

4996997 seqs, 3332346308 residues Searched:

9993994 Total number of hits satisfying chosen parameters:

seq length: 0 seq length: 200000000 Minimum DB E Maximum DB E Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

geneseqn2001bs:*
geneseqn2002as:*
geneseqn2002bs:*
geneseqn2003as:*
geneseqn2003as:* geneseqn1980s:* geneseqn1990s:* geneseqn2000s:* geneseqn2001as:* geneseqn2003cs:* geneseqn2003ds:* geneseqn2004as:* geneseqn2004bs:* N Geneseq 21:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

geneseqn2005s:*

SUMMARIES

					COLUMNICA	
		de				
Result		Query				
No.	Score	Match	Match Length DB	BB	ΙD	Description
-1	24.2	60.5	145985	12	ADQ97164	Adq97164 Human can
7	23.2	58.0	881	9	ABN98755	Abn98755 Arabidops
m	22.6	56.5	413	12	ADQ17678	Adq17678 Human sof
4	22.6	56.5	2091	9	ABQ76538	Abq76538 C. albica
υ Ω	22.2	55.5	1107	Ŋ	AAH66350	Aah66350 C glutami
y U	22.2	55.5	1164	ω	ACA00491	Aca00491 C. glutam
C 7	22.2	55.5	1230	14	AEB15386	Aeb15386 C glutami
ω υ	22.2	55.5	1294	10	ADD13935	Add13935 C. glutam
o o	22.2	55.5	1600	9	AAL46365	Aal46365 C glutami
c 10	22.2	55.5	349980	Ŋ	AAH68528	Aah68528 C glutami
c 11	22	55.0	564	8	ABZ53923	Abz53923 Aspergill
c 12	21.6	54.0	882	0	ADA29579	Ada29579 DNA encod
13	21.6	54.0	100660	13	ABD32721 3	Continuation (4 of
C 14	21.4	53.5	1296	4	AAH46906 _	Aah46906 cDNA enco
c 15	21.4	53.5	1628	13	ADX51526	Adx51526 Plant ful
c 16	21.4	53.5	1842	ហ	AAS87541	Aas87541 DNA encod
17	21.4	53.5	2378	14	ADZ60316	Adz60316 Murine Ey
c 18	21.2	53.0	282	0	AAT32713	Aat32713 Sequence
c 19	21.2	53.0	334	7	AAT32716	Aat32716 Third Ig

Abz51404 Aspergill Aca45110 Huwan gen Aaf13052 Aspergill Ada50596 Aspergill Ada505096 Aspergill Aca28075 Prokaryot Asf84800 Nucleotid Aax11856 Human bia Aca54523 Prokaryot Aax54847 Human Cyc Aax1686 Nucleotid Aca56533 Human Cyc Aax65468 Nucleotid Acd26033 Human Cyc Ada60163 Transgeni Aca56597 Aspergill Ach56597 Aspergill Ach56597 Aspergill Ach56597 Aspergill Ach56497 Aspergill Ach8640 Cotton gy Acn523 Acpergill Ach8640 Cotton gy Acn52424 Cotton gy Ach5640 Cotton gy Ach5663 Cotton gy	Aaf13911 Aspergill Adu57952 Aspergill
ABZ51404 AACW45110 AACW5110 AACW5110 AAF13052 AAF13052 ADU57093 AAX78075 AAX78075 AAX78247 AAX78247 AAX78247 AAX86503 ADO14234 ADO14234 ADO16033 ADR85697 ADR85697 ADR85510 ADR85510 ADR85510 ADR84523 ACN58640 ACN58640	AAF13911 ADU57952
0 4 4 6 4 7 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8	13
122143 22143 22143 6337 6337 6337 10001 1200 23360 23360 23560 2550 2550 2550 2550 2550 2550 2550 2	0 6 8 3 0 6 8 3 0 6 8 3
	51.0
	20.00
¼	יסיטי
00000000000000000000000000000000000000	202
01222222222222222222222222222222222222	44 6
	000

ALIGNMENTS

AD097164 standard; DNA; 145985 BP (first entry) 07-OCT-2004 ADQ97164; RESULT 1 ADQ97164

Cytostatic; Gene Therapy; cancer; leukemia; lymphoma; Human; ds Human cancer associated sequence HD1-08-009, SEQ ID 140.

Homo sapiens.

WO2004060304-A2.

22-JUL-2004

22-DEC-2003; 2003WO-US041389.

27-DEC-2002; 2002US-00330773.

(SAGR-) SAGRES DISCOVERY INC.

Morris DW, Malandro MS;

WPI; 2004-543781/52.

New isolated cancer associated nucleic acids comprising at least 10 contiguous nucleotides, useful for diagnosing, preventing and/or treating cancers such as leukemia and lymphoma.

Claim 1; SEQ ID NO 140; 199pp; English

The present invention relates to cancer associated sequences (ADQ97025-ADQ98004). The sequences are useful for the diagnosis, prevention and/or treatment of cancer, such as leukemia and lymphoma. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic formate directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.

Sequence 145985 BP; 40325 A; 30740 C; 31191 G; 43391 T; 0 U; 338 Other;

~

```
셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ð
                                                            °
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The invention relates to an Arabidopsis thaliana nucleic acid (I) comprising a sequence capable of hybridising under stringent conditions to a sequence selected from any one of 999 sequences (ABN98233-ABN99231), given in the specification or its fragment. A polypeptide (II) encoded by (I), a transgent plant (III) comprishing an exogenous nucleic acid or a genetically modified cell (IV) comprising an exogenous nucleic acid, is
                                                                                                                                                                                                                                                                                                                                                                                                                      Arabidopsis thaliana; plant; insecticide; fungicide; transgenic; stress; disease; crop; thale cress; tolerance factor; insect; pathogen; nutrition; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New Arabidopsis thaliana nucleic acid for identifying homologous genes, producing compositions that modulate the expression or function of its encoded protein, and mapping functional regions of protein.
                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Haas WD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ledford BL, Woesener JP, Haas V
Davis KR, Allen K, Hoffman N;
                     DB 12; Length 145985;
                                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Yu Y;
                                                                                                                                                                                                                                                                                                                                                                               Arabidopsis thaliana expressed polynucleotide SEQ ID NO 523
                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 1; SEQ ID NO 523; 49pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Raines TM,
                                                                                                                                           88582 Grigoricaraninaccandacriciriogcadiag 88618
                                                                                                      40
                                                            œ
                                                                                                      4 GCTGCTTGGTCAGACTTATCCAGATTCTTGGCGGTAG
                 Score 24.2; DE Pred. No. 17; 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Price JL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mathew AV,
1, Slater T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            An Y, Hamilton CM,
                                                                                                                                                                                                                                                   ABN98755 standard; DNA; 881 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   26-JAN-2001; 2001US-00770445.
                 Query Match
Best Local Similarity 78.4%;
Matches 29; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              27-JAN-2000; 2000US-0178472P
                                                                                                                                                                                                                                                                                                                                      (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Garcia CA, Kricker M,
Hurban P;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LEDFORD B L.
WOESSNER J P.
HAAS W D.
GARCIA C A.
KRICKER M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Arabidopsis thaliana.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          HAMILTON C M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Page A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2002-403163/43.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RAMEAKA J G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRICE J L.
RAINES T M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PAGE A.
MATHEW A V.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GORLACH J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HOFFMAN N.
HURBAN P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ц.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DAVIS K FALLEN K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US2002023281-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gorlach J, A
Rameaka JG,
                                                                                                                                                                                                                                                                                                                                      01-AUG-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            21-FEB-2002
                                                                                                                                                                                                                                                                                            ABN98755;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (PRIC/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ALLE/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HURB/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              <u>xax</u>/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RAME/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PAGE/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MATH/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LEDF/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (HAAS/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (GARC/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               KRIC/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SLAT/)
                                                                                                                                                                                                          RESULT 2
ABN98755
AND ABN98755
AND ABN98755
AND ABN9
AXX ARBN9
AXX
                                                                                                                                         셤
                                                                                                        ò
```

```
useful for screening a candidate agent for its biological effect. (I) is useful in identifying homologous or related genes, in producing compositions that modulate the expression or function of its encoded protein, mapping functional regions of the protein and in studying associated physiological pathways. (I) is also useful for the genetic commonitation of cells, particularly plant cells. (I) is also useful in screening assays of various plant strains to determine the strains that are best capable of withsteading a particular disease or environmental stress. (II) and (III) are useful for screening of biologically active agents, e.g. fungicides, insecticides, etc., for elucidating blochemical pathways. The screened agents are useful in improved methods of treating crops to prevent or treat disease. (II) are also useful in screening of programs to identify agents that mimic or enhance the action of tolerance (factors. Such agents are useful in improved methods of treating crops to programs to identify production of a biosynthetic product in a plant. (III) is useful for identifying other mediators that may induce expression of proteins of interest, for establishing the extent to which any specific insect and/or pathogen is responsable for damage to a particular plant, for identifying other mediators that enhance or induce to environmental stress, for identifying factors involved in construction of the study of genetic function and regulation, or and crimal value and for identifying productions of nutritional, commercial or medicinal value and constrained to the scullular metabolism and for screening compounds that may affect the biological function of the gene or gene products. Note: The sequence data for this parent did not form part of the printed or products.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               soft tissue sarcoma; cytostatic; gene therapy; vaccine; screening; human;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Early detection of soft tissue sarcoma comprises determining expression of a gene in a first soft tissue sample and a normal soft tissue sample and comparing the gene expression, also useful in treating soft tissue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 23.2; DB 6; Length 881; Pred. No. 14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 881 BP; 251 A; 154 C; 206 G; 268 T; 0 U; 2 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human soft tissue sarcoma-upregulated DNA - SEQ ID 495.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       at segdata.uspto.gov/sequence.html?DocID=99999770445
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      177 AGCTGCAATGTCATACTTATCAGGTTTCTTGGAGGT 212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3 AGCTGCTTGGTCAGACTTATCCAGATTCTTGGCGGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Zlotnik A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (PROT-) PROTEIN DESIGN LABS INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 26-NOV-2002; 2002US-0429739P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      58.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         26-NOV-2003; 2003WO-US038193.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADQ17678 standard; DNA; 413
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               26-AUG-2004 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        28; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Aziz N, Ginsburg WM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2004-441208/41.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WO2004048938-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 10-JUN-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADQ17678;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 3
```

```
The invention relates to a novel method for detecting soft tissue sarcoma which comprises obtaining a first soft tissue sample from an individual and a normal soft tissue sample from the same or different individual, determining the expression of a gene in both samples and comparing the expression of the gene in both soft tissue samples, where a higher level of protein expression in the first soft tissue sample indicates the
                                                                                                                                                                                                                                                                                     presence of soft tissue sarcoma. The method of the invention has cytostatic applications and may be useful for detecting soft tissue sarcoma, possibly via gene therapy or vaccine production. The nucleic acid sequences may be useful in diagnostic and screening applications. The current sequence is that of a human soft tissue sarcoma-upregulated DNA of the invention. The current sequence is not shown within the specification per se but was submitted in CD format by the inventor.
                                                         Example 2; SEQ ID NO 495; 210pp; English.
#X%XCCCCCCCCCCXX
```

Sequence 413 BP; 108 A; 106 C; 72 G; 127 T; 0 U; 0 Other;

Gaps ö DB 12; Length 413; Indels 276 cadericererececacerearecadarrerreced 6 2 GAGCTGCTTGGTCAGACTTATCCAGATTCTTGGCGGT 38 Pred. No. 21; 0; Mismatches Score 22.6; Pred. No. 21 56.5%; Local Similarity 75.7 les 28; Conservative Query Match Matches ઠે

ö

ABQ76538 standard; cDNA; 2091 BP

ABQ76538;

(first entry) 21-NOV-2002 C. albicans BAX-associated cDNA fragment SEQ ID 501.

Bax; Bax-resistance; cytostatic; fungicide; immunosuppressive; virucide; vasotropic; vaccine; gene therapy; proliferative disorder; cancer; apoptosis; fungal; yeast; infection; autoimmune disease; ischaemia; neurodegeneration; cell death; ss.

Candida albicans

WO200264766-A2.

22-AUG-2002

21-DEC-2001; 2001WO-EP015398.

22-DEC-2000; 2000EP-00870318. 04-JAN-2001; 2001EP-00870002. 09-JAN-2001; 2001EP-00870003.

(JANC) JANSSEN PHARM NV

Contreras RH, Bberhardt I, Luyten WHML, Reekmans RJ; WPI; 2002-667002/71. P-PSDB; ABG93272

isolated nucleic acid representing a synthetic BAX-gene, useful as

medicament for treating, preventing and/or alleviating yeast or fungal infections or proliferative disorders, or for preventing apoptosis in

or fungal

Claim 36; Fig 2; 344pp; English.

certain diseases

This invention describes a novel nucleic acid representing a synthetic Bax gene. The Bax gene of the invention is useful for identifying Bax-resistant yeast or fungi, identifying, or obtaining and identifying

Candida spp. sequences that are differentially expressed in a pathway eventually leading to programmed cell death or identifying inhibitors or inhibitors sequences of bax-induced cell death. The products of the inhibitor sequences of bax-induced cell death. The products of the invention have cytostatic, fungicide; imminosuppressive, virucide and vasotropic activity and can be used in vaccines or for gene therapy. The contisense molecules and antibodies useful as medicament or in preparing a medicament for treating, preventing and/or alleviating contisense, or for preventing apoptosis in certain diseases. Such as cancer, or for preventing apoptosis in certain diseases. The compounds or polypeptides, or the genetically modified organism are useful for preparing a medicament for modifying the endogenic flora of humans and conther mammals. The vaccine is useful for immunisting against yeast or fungal infections. Apoptosis-related diseases include autoimmune disease. This sequence represents a polynucieotide associated with the Bax gene ö Gaps ö DB 6; Length 2091; Sequence 2091 BP; 725 A; 384 C; 430 G; 552 T; 0 U; 0 Other; Indels 6 described in the disclosure of the invention Score 22.6; DE
Pred. No. 30;
O; Mismatches 56.5%; Query Match Best Local Similarity 75.7 Matches 28; Conservative

셤 8

RESULT 5

AAH66350 standard; DNA; 1107 BP AAH66350;

(first entry) 26-SEP-2001 C glutamicum coding sequence fragment SEQ ID NO: 1385.

Coryneform bacterium; amino acid synthesis; vitamin; saccharide; organic acid synthesis; ds.

Corynebacterium glutamicum.

EP1108790-A2.

20-JUN-2001

18-DEC-2000; 2000EP-00127688

99JP-00377484. 2000JP-00159162 16-DEC-1999; 07-APR-2000;

03-AUG-2000; 2000JP-00280988.

(KYOW) KYOWA HAKKO KOGYO KK

S, Hayashi M, Ochiai K, Yokoi H; Ozaki A; H, Ando S, Ikeda M, O Mizoguchi Senoh A, Nakagawa S, Tateishi N,

WPI; 2001-376931/40.

P-PSDB; AAG91131.

mutation point of a gene, measuring expression of a gene, analyzing expression profile or pattern of a gene and identifying homologous gene. Novel polynucleotides derived from Coryneform bacteria, for identifying

Claim 8; SEQ ID NO 1385; 246pp + Sequence Listing; English.

The present invention provides a number of nucleotide and protein sequences from the Coryneform bacterium Corynebacterium glutamicum. These rate useful for identifying the mutation point of a gene derived from a mutant of coryneform bacterium, messuring expression amount and analysing the expression profile or expression pattern of a gene derived from

AEB15386/c ID AEB15386 standard; DNA; 1230 BP.

RESULT 7

(first entry)

22-SEP-2005

ö

AEB15386;

```
Corynebacterium glutamicum polynucleotides. The arrays are used to analyse C. glutamicum, particularly for monitoring a fermentation process to determine expression levels of C. glutamicum cellular mRNA. Such monitoring particularly differentiates between expression levels of moliferent strains of C. glutamicum and allows the adjustment of different culture and fermentation conditions. ACA00010-ACA02188 represent C. glutamicum derived polynucleotides described in the disclosure of the
Coryneform bacterium, and identifying a homologue of a gene derived from coryneform bacterium. Coryneform bacteria are useful for producing amino acids, nucleic acids, vitamins, saccharides and organic acids, particularly L-lysine. The present sequence is a nucleic acid described in the exemplification of the invention. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from the European Patent Office
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New nucleic acid array useful for monitoring mRNA expression of Corynebacterium glutamicum during fermentation, comprising nucleic acid from Corynebacterium glutamicum.
                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                         ô
                                                                                                                                                                                                                                                                                   Length 1107;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This invention describes a novel nucleic acid array involving
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pfefferle W, Bathe B, Huthmacher K;
                                                                                                                                                                                                                            Seguence 1107 BP; 288 A; 296 C; 288 G; 235 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 1164 BP; 302 A; 308 C; 302 G; 252 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Coryneform; nucleic acid array; fermentation; culture; ds.
                                                                                                                                                                                                                                                                                                                                         3; Indels
                                                                                                                                                                                                                                                                                      ŝ
                                                                                                                                                                                                                                                                                   8
                                                                                                                                                                                                                                                                                Score 22.2; DE
Pred. No. 39;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                   704 ccercararccaearrcrreecerae 678
                                                                                                                                                                                                                                                                                                                                                                                             14 CAGACTTATCCAGATTCTTGGCGGTAG 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C. glutamicum derived ORF SEQ ID 482.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 6
ACA00491/C
ID ACA00491 standard; DNA; 1164 BP.
XX
ACA00491;
XX
ACA00491;
XX
C 2-JUN-2003 (first entry)
XX
XX
C 3-JUN-2003 (first entry)
XX
C COTYNEBACTERIUM GLUTAMICUM.
XX
C COTYNEBACTERIUM GLUTAMICUM.
XX
DE10128510-A1.
XX
PD 19-DEC-2002.
XX
PP 13-JUN-2001; 2001DE-01028510.
XX
PP 13-JUN-2001; 2001DE-01028510.
XX
PP 13-JUN-2001; 2001DE-01028510.
XX
PY 13-JUN-2001; 2001DE-01028510.
XX
PY 13-JUN-2001; 2001DE-01028510.
XX
PY New nucleic acid array useful for Corynebacterium glutamicum during PT Corynebacterium glutamicum.
XX
XX
New nucleic acid array useful for Corynebacterium glutamicum during PT Corynebacterium glutamicum.
XX
XX
New nucleic acid array useful for Corynebacterium glutamicum during PT Corynebacterium glutamicum.
XX
C This invention describes a novel n Corynebacterium glutamicum, particularly differenti condition condition glutamicum derived polymucleotides
CC culture and fermentation condition
CC Invention
XX
C Sequence 1164 BP; 302 A; 308 C; 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 1; Page 221; 709pp; German.
                                                                                                                                                                                                                                                                                      55.54;
                                                                                                                                                                                                                                                                                                                                         24; Conservative
                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                            Matches
     88888888888
                                                                                                                                                                                                                                                                                                                                                                                                                                             셤
                                                                                                                                                                                                                                                                                                                                                                                                8
```

```
This invention relates to novel isolated metabolic pathway regulatory polypeptides from Corynebacterium glutamicum, designated MR proteins, and the DNA sequences which encode them. The invention is useful in identification of C glutamicum and related organisms, mapping of genomes of organisms related to C glutamicum, identification and localization of C glutamicum sequences of interest, evolutionary studies, determination of MR protein regions required for function, modulation of MR protein as a fine chemical. The present sequence is that of a gene which encodes a novel isolated metabolic pathway regulatory polypeptide of the invention from Corynebacterium glutamicum. Note: This sequence does not directly from USPTO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           An isolated metabolic pathway regulatory polypeptide from Corynebacterium glutamicum, its portion, or its variant, useful for diagnosing presence
                                                                     C glutamicum metabolic pathway regulatory protein-encoding gene SeqID301.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                 metabolism; microorganism detection; microorganism identification; genome; evolution; protein production; gene; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               55.5%; Score 22.2; DB 14; Length 1230; 88.9%; Pred. No. 40; ive 0; Mismatches 3; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 1230 BP; 323 A; 320 C; 320 G; 267 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Haberhauer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Schroder H, Zelder O,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          glutamicum, its portion, or its variant, or activity of C. diphtheriae in subject.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 1; SEQ ID NO 301; 65pp; English.
                                                                                                                                                                                                                                                                                                                                 99DE-01032122.
99DE-01032128.
99DE-01032134.
                                                                                                                                                                                                                                 06-DEC-2004; 2004US-00006098.
                                                                                                                                                                                                                                                             99US-0141031P
                                                                                                                                                                                                                                                                                                                                                                                                                                    99DE-01041390.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 99DE-01042124
                                                                                                                                                                                                                                                                                                                                                                           99DE-01032206
                                                                                                                                                                                                                                                                                                                                                                                                        99DE-01033003
                                                                                                                                                                                                                                                                                                                                                                                                                        99US-0151251P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                23-JUN-2000; 2000US-00602874
                                                                                                                                                                                                                                                                                                       99DE-01031419
                                                                                                                                                                                                                                                                                                                     99DE-01031420
                                                                                                                                                                                                                                                                                                                                                                                            99DE-01032207
                                                                                                                                           Corynebacterium glutamicum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity 88.9
Matches 24; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ď
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2005-496831/50.
P-PSDB; AEB15387.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pompejus M, Kroger
                                                                                                                                                                         US2005153402-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (BADI ) BASF AG.
                                                                                                                                                                                                                                                                                                                                                   999;
                                                                                                                                                                                                                                                                                                                                                                                                           999;
                                                                                                                                                                                                    14-JUL-2005
                                                                                                                                                                                                                                                                                                                                                                                                                                                  03-SEP-1999,
                                                                                                                                                                                                                                                                                                                                                                              999
                                                                                                                                                                                                                                                                                                                                 09-JUL-1
                                                                                                                                                                                                                                                                                                                                                              09-JUL-1
09-JUL-1
09-JUL-1
                                                                                                                                                                                                                                                                                                                                                                                                                        7-AUG-1
                                                                                                                                                                                                                                                                                                                                                                                                        14-JUL-
```

14 CAGACTTATCCAGATTCTTGGCGGTAG 40

8

ö

Gaps

ö

Indels

3,

40

Score 22.2; DE Pred. No. 39; 0; Mismatches

55.5%; ilarity 88.9%; Conservative

Local Similarity hes 24; Conser

Query Match Best Loca Matches 761 ccercararccagarrerresceras 735

셤

ઠે

14 CAGACTTATCCAGATTCTTGGCGGTAG

DB 8; Length 1164;

```
This invention describes novel polymucleotides and polypeptides that are involved in metabolic regulation, i.e. in transcriptional and (post) translational regulation of metabolic proteins in Corynebacterium (glutamicum. Polymucleotides are isolated from a nucleic acid library of c. glutamicum then mutated a specified positions, cloned and expressed by standard methods. Cells, containing vectors that express the polymucleotides are used for production of fine chemicals, preferably amino acids and specifically lyshine, but more generally nucleotides, nucleosides, lipids, fatty acids, diols, carbohydrates, aromatic compounds, vitamins, co-factors and enzymes. These are useful in the companies, optionally as primers and probes, can also be used for identification and classification of c. glutamicum and related species, c.g. for diagnosis, for genomic mapping, functional or evolutionary studies, gene manipulation, and modulation of metabolic activity. Cells that contain the polymucleotides of the invention may produce fine c.g. chemicals in better yields, with higher productivity and/or more
                                                                                                                                                                                                                                                               de; gene; metabolic regulation; fine chemical production; amino acid production; lysine production; nucleotide production; nucleoside production; nucleoside production; lipid production; fatty acid production; carbohydrate production; aromatic compound production; vitamin production; co-factor production; enzyme production; food; animal feed; cosmetic; pharmaceutical.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New nucleic acid encoding variant forms of metabolic regulatory useful for production of fine chemicals, specifically lysine, in microorganisms.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Schroeder H, Kroeger B, Klopprogge C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 1294 BP; 339 A; 336 C; 334 G; 285 T; 0 U; 0 Other;

    C. glutamicum regulatory associated DNA RXA00205.

804 CCGTCATATCCAGATTCTTGGCGGTAG 778
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 1; SEQ ID NO 1; 164pp; German.
                                                                                                                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers
                                                                                                                  ADD13935 standard; DNA; 1294 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    31-OCT-2002; 2002WO-EP012139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        05-NOV-2001; 2001DE-01054245
                                                                                                                                                                                                                                                                                                                                                                                                          Corynebacterium glutamicum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   101. .1267
                                                                                                                                                                                              (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pompejus M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2003-532615/50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            P-PSDB; ADD13936
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WO2003040181-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (BADI ) BASF AG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Haberhauer G;
                                                                                                                                                                                              01-JAN-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            15-MAY-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   zelder O,
                                                                                                                                                        ADD13935;
```

```
The present invention provides the protein and coding sequences of the Corynebacterium glutamicum ccpAl gene. The sequences can be used in the production of L form amino acids, particularly L-lysine, which are useful in human medicine, the pharmaceutical and food industries and, particularly, in animal nutrition. The present sequence is the gene of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New ccpAl gene from coryneform bacteria, useful, when suppressed, for
increasing fermentative production of L-amino acids, particularly lysine.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                          Coryneform bacteria; ccpA1; L amino acid production; L-lysine; gene; animal nutrition; medicine; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 6; Length 1600;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 1600 BP; 407 A; 396 C; 423 G; 374 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C glutamicum coding sequence fragment SEQ ID NO: 7063.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 22.2; DE
Pred. No. 42;
0; Mismatches
            985 ccercararccadarrerredecerad 959
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          14 CAGACTTATCCAGATTCTTGGCGGTAG 40
40
14 CAGACTTATCCAGATTCTTGGCGGTAG
                                                                                                                                                                                                                                                         Location/Qualifiers
225. .1391
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 4; Page 10-12; 16pp; German.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BP
                                                                                                                                                                                                                                                                                    /*tag= a
/product= "ccpA1"
                                                                                       AAL46365 standard; DNA; 1600 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAH68528 standard; DNA; 349980
                                                                                                                                                                                                                                                                                                                                                                            02-MAR-2001; 2001DE-01010052
                                                                                                                                                                                                                                                                                                                                                                                                      26-AUG-2000; 2000DE-01042054
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Match 55.5%;
Local Similarity 88.9%;
les 24; Conservative
                                                                                                                                                                                                                                 Corynebacterium glutamicum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
                                                                                                                                         (first entry)
                                                                                                                                                                   C glutamicum ccpAl gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Moeckel B, Kreutzer C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2002-363944/40.
P-PSDB; AAO17531.
                                                                                                                                                                                                                                                                                                                                                                                                                               (DEGS ) DEGUSSA AG
                                                                                                                                                                                                                                                                                                                           DE10110052-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      the invention
                                                                                                                                         19-JUL-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      26-SEP-2001
                                                                                                                                                                                                                                                                                                                                                    07-MAR-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New ccpA1
                                                                                                                 AAL46365;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAH68528
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best Loca
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 10
AAH68528/C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                XXXXX
                                                                                                                 Š
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  셤
                    셤
ò
```

proteins,

ö

ö

Gaps

ö

th 55.5%; Score 22.2; DB 10; Length 1294; Similarity 88.9%; Pred. No. 40; 24; Conservative 0; Mismatches 3; Indels 0;

Best Local Similarity

Query Match Matches Horiuchi H; Abe K;

```
The invention relates to a polynucleotide having any of 6006 specific sequences (ABZ5088-ABZ56893), which are expressed by a fungus under specific culture conditions including one or more of eutrophic, oligotrophic, solid, early germination, alkaline, high temperature, low temperature or maltose culture or polynucleotides stringently hybridising progress of fermentation and the growth conditions of a fungus, especially of Aspergillus oryzae which is widely used in industrial fermentation. Also monitoring for fungal contamination. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New Acinetobacter baumanii proteins and nucleic acids, useful as reagents for diagnosing a bacterial disease, as components of antibacterial
                                                                                                                                                                                                                                                                    Detection of expression of specific Aspergillus genes for monitoring the fermentation and growth conditions of the fungus, using DNA probes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               gene; Acinetobacter baumannii; bacterial disease; antibacterial;
                                                                                                                                                                                                                                                                                                                                        Claim 1; SEQ ID NO 3036; 48pp + Sequence Listing; Japanese
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 22; DB 8; Length 564; Pred. No. 41;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 564 BP; 127 A; 166 C; 126 G; 145 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Mismatches 10; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  429 AGCATCTTCGTCGGATTTTTCCATACTCTTGGCAGAAG 392
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3 AGCTGCTTGGTCAGACTTATCCAGATTCTTGGCGGTAG 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DNA encoding Acinetobacter baumannii protein #866.
                                                                                                                                                       Akita O, Kashiwagi Y, Kitamoto K,
Kobayashi T, Kitamoto N, Gomi K,
                                                             NAT INST ADVANCED IND SCI & TECHNOLOGY.
NAT RES INST BREWING.
NAT FOOD RES INST MIN AGRIC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (GENO-) GENOME THERAPEUTICS CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           vaccine; plant biocontrol agent
                     30-MAR-2001; 2001JP-00098371.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            99US-00328352.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         98US-0088701P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 55.0%;
Best Local Similarity 73.7%;
Matches 28; Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADA29579 standard; DNA; 885
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Acinetobacter baumannii.
                                                                                                                                                         Akita O,
                                                                                                                                                                                                                       WPI; 2003-046817/04.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2003-576092/54 P-PSDB; ADA33705.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Breton G, Bush D;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            04-JUN-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         09-JUN-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            20-NOV-2003
                                                                                                                                                                               rakeuchi M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US6562958-B1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  13-MAY-2003.
                                                                                                                                                         Machida M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADA29579;
                                                               (NAAD-)
                                                                                                            (NORQ )
                                                                                     NARE-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADA29579/
유
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The present invention provides a number of nucleotide and protein sequences from the Coryneform bacterium Corynebacterium glutamicum. These are useful for identifying the mutation point of a gene derived from a mutant of coryneform bacterium, measuring expression amount and analysing the expression profile or expression pattern of a gene derived from Coryneform bacterium, and identifying a homologue of a gene derived from coryneform bacterium. Coryneform bacteria are useful for producing amino acids, nucleic acids, vitamins, saccharides and organic acids, particularly L-lysine. The present sequence is a nucleic acid described in the exemplification of the invention. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from the European Patent Office
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               mutation point of a gene, measuring expression of a gene, analyzing expression profile or pattern of a gene and identifying homologous gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Novel polynucleotides derived from Coryneform bacteria, for identifying mutation point of a gene, measuring expression of a gene, analyzing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 349980 BP; 80727 A; 91049 C; 97618 G; 80586 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                             Yokoi H;
                  Coryneform bacterium; amino acid synthesis; vitamin; saccharide; organic acid synthesis; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     55.5%; Score 22.2; DB 5; Length 349980; 88.9%; Pred, No. 1.4e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Disclosure, SEQ ID NO 7063; 246pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Aspergillus oryzae; fermentation; fungus; industrial; EST; expressed sequence tag; gene; ss.
                                                                                                                                                                                                                                                                                                                                                                                                           Ando S, Hayashi M, Ochiai K,
da M, Ozaki A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         <u>ب</u>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Aspergillus oryzae polynucleotide SEQ ID NO 3036
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              117041 CCGTCATATCCAGATTCTTGGCGGTAG 117015
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   14 CAGACTTATCCAGATTCTTGGCGGTAG 40
                                                                                                                                                                                                                                                                                                                                                                                                           Nakagawa S, Mizoguchi H, Ando :
Tateishi N, Senoh A, Ikeda M,
                                                                                                                                                                                                                                                                    16-DEC-1999; 99JP-00377484.
07-APR-2000; 2000JP-00159162.
03-AUG-2000; 2000JP-00280988.
                                                                                                                                                                                                                            18-DEC-2000; 2000EP-00127688
                                                                                                                                                                                                                                                                                                                                                              (KYOW ) KYOWA HAKKO KOGYO KK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ABZ53923 standard; cDNA; 564
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     22-MAR-2002; 2002WO-IB000890.
                                                                                       Corynebacterium glutamicum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       24; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2001-376931/40.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Aspergillus oryzae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WO200279476-A1.
                                                                                                                                  EP1108790-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       28-MAR-2003
                                                                                                                                                                               20-JUN-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           10-OCT-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ABZ53923;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
```

Matches

ò 셤 ö

Gaps

ö

```
c disorder and polymucleotides encoding the polypeptides. The kinase cissor and polymucleotides encoding the polypeptides. The kinase c disorder such as cancer, immune-related diseases, cardiovacular disease, brain or neuronal-associated disease and metabolic disorders, including cancers of tissues, cancers of hematopoietic origin, diseases of the central nervous system, diseases of the peripheral nervous system, diseases of the peripheral nervous system, contral nervous system, diseases of the peripheral nervous system, contral infections, infections caused by prions, alteral sclerosis, viral infections, infections caused by prions, conditions, and order of metabolic disorders, attention disorders, neurological disorders, dyskinesias, hypertension, psychotic disorders, neurological disorders, dyskinesias, concading rhinitis, autoimmunity, atherosclerosis, psoriasis, costecathritis, asthma, chronic inflammatory bowel disease, theumatory pelvic disorders and sistension, costecathritis, asthma, chronic inflammatory bowel disease, clothing disorders and attention as glaucoma, retinopathy and macular describing in disorders and attention as glaucoma, retinopathy and macular describing in gene conlar diseases such as glaucoma, retinopathy and macular describing the configuration, etc. The polymucleotides are useful in gene contar dementia, manic depression, etc. The polymucleotides are useful in gene contar through the children in the above mentioned disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      plant protectant; plant growth regulant; gene therapy; plant; recombinant DNA construct; physical array; plant breeding marker; cold tolerance; heat tolerance; drought tolerance, herbicide tolerance; extreme osmotic condition; pathogen tolerance; pest tolerance; growth rate; cell cycle pathway; disease resistance; galactomannan production; lignin production; plant growth regulator; yield; plant growth; plant development; seed oil; protein yield;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAH46891-46922 represent human protein kinases encoding cDNA molecules
                                                                                                                                                                                                                                                                                                                                                    Kinase polypeptides useful for treating cancers, Alzheimer's disease, viral infections, diabetes, obesity, organ transplant rejection and rheumatoid arthritis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The invention provides human protein kinases and protein kinase-like
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       53.5%; Score 21.4; DB 4; Length 1296; 80.6%; Pred. No. 89;
                                                                                                                                                                                                                                        Manning G, Sudarsanam S, Martinez R;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 1296 BP; 340 A; 342 C; 339 G; 273 T; 0 U; 2 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indele
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Plant full length insert polynucleotide seqid 26266.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ..
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              415 GAGCTGCTTACTTATACTTCTCCACATTCTT 385
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2 GAGCTGCTTGGTCAGACTTATCCAGATTCTT 32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Example 1; Page 206; 218pp; English.
                                        31-JAN-2000; 2000US-0179364P.
17-PEB-2000; 2000US-0183173P
17-MAR-2000; 2000US-0190162P.
29-MAR-2000; 2000US-019404P.
13-NOV-2000; 2000US-0247013P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADX51526 standard; cDNA; 1628
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               21-APR-2005 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity 80.6
hes 25; Conservative
                                                                                                                                                                                                                                        Plowman G, Whyte D,
                                                                                                                                                                                                                                                                                     WPI; 2001-476202/51.
P-PSDB; AAB85506.
                                                                                                                                                                                           (SUGE-) SUGEN INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADX51526;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Loca
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADX51526/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 15
  ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            from base 300001 (Human cancer-associated genomic DNA LOCUS ABD32721 Accession Abd32721
                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Protein kinase; enzyme; cytostatic; nootropic; neuroprotective; human; antiparkinsonian; virucide; antibacterial; antifungal; antimigraine; antipacis; hypotensive; hypertensive; immunosuppressive; antiallergic; antipaciatic; antixheumatic; antiarthritic; ophthalmological; anorectic; osteopathic; thrombolytic; antiarteriosclerotic; antiasthmatic; vasotropic; antidiabetic; gene therapy; ss.
targets for antibacterial drugs, or as biocontrol agents for
                                                                                                                The invention relates to isolated Acinetobacter baumannii nucleic acids. The A. baumannii nucleic acids and polypeptides are useful as reagents for diagnosing a bacterial disease, as components of antibacterial vaccines, as targets for antibacterial drugs, to detect the presence of A. baumannii and other Acinetobacter species in a sample, in screening compounds for the ability to interfere with the A. baumannii life cycle or to inhibit A. baumannii infection, and as biocontrol agents for plants. The present sequence represents DNA encoding an A. baumannii
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gapa
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 13; Length 100660;
                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 75.0%; Pred. No. 67;
Matches 27; Conservative 0; Mismatches 9; Indels
                                                                                                                                                                                                                                                                                                                                                           Sequence 885 BP; 273 A; 166 C; 203 G; 243 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       79432 GIGCIGCTIGGTTAGAATTTTGAAGATTCTTCTCAG 79467
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         260 GCTTCACGTCAGACACATCAAGCTTTTTGGTGGTA 225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ę,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          4 GCTGCTTGGTCAGACTTATCCAGATTCTTGGCGGTA 39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 21.6; DB 1
Pred. No. 2e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2 GAGCTGCTTGGTCAGACTTATCCAGATTCTTGGCGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             cDNA encoding human protein kinase SGK090
                                                                      Example; SEQ ID NO 866; 328pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     110000
210000
310000
400660
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Location/Qualifiers
1. .1293
/*tag= a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             906/c
AAH46906 standard; cDNA; 1296 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             fragments
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               25-JAN-2001; 2001WO-US002337.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ABD32721
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ch 54.0%;
1 Similarity 75.0%;
27; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              100001
200001
300001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Begin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ABD32721_3
Continuation (4 of 4) of AB
WP Sequence split into 4 fr
WP Pragment Name B
WP ABD32721_0
WP ABD32721_2
WP ABD32721_2
WP ABD32721_3 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Fragment Name
ABD32721 0
ABD32721 1
ABD32721 2
ABD32721 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WO200155356-A2
  vaccines, as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             25-SBP-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               02-AUG-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAH46906;
                                                                                                                                                                                                                                                                                                                 protein.
                           plants
```

Matches

셤

ઢ

RESULT 13

셤

ઠ

ö

Gaps

ö

```
The invention describes a recombinant DNA construct comprising a polymucleotide consisting of a sequence encoding an amino acid sequence available in electronic form from the US patent office at the invention are also useful in physical arrays of molecules and as plant breeding markers. The recombinant DNA construct is useful for improving plant tolerance to cold, heat, drought, herbicides, extreme camporate by modification of the cell cycle pathway, for conferring increased resistance to plant disease, for manipulating growth rate in plant or plant growth regulators, for manipulating growth rate in increased resistance to plant disease, for producing galactomannan, lighin or plant growth regulators, for increasing the rate of homologous recombination in plants, for improving yield by modification of photosynthesis or carbohydrate, introgen or phosphorus use and/or uptake or by providing improved plant growth and development under at least one stream of the capture or plant full length insert content. This sequence represents a plant full length insert of the plant can be used in the recombinant DNA construct of the
                                                                                                                                                                                                                                                                                                                                                                                                                        New recombinant DNA construct, useful for improving plant tolerance to cold, heat, drought, herbicides, extreme osmotic conditions, pathogens or pests, for conferring increased resistance to plant disease, or for improving yield.
                                                                                                                                                                                                                                                                                                                                                          Cao Y;
                                                                                                                                                                                                                                                                                                                                                        Tabaska JE,
                                                                                                                                                                                                                                                                                                                                                        Liu J, Zhou Y, Kovalic DK, Screen SE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 1; SEQ ID NO 26266; 15pp; English.
                                                                                                                                          28-APR-2003; 2003US-00425114.
                                                                                                                                                                           06-MAY-1999; 99US-00304517.
 protein content; gene; ss
                                                                                                                                                                                                                             LIU J.
ZHOU Y.
KOVALIC D K.
SCREEN S E.
TABASKA J E.
                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2004-180133/17.
                                                                      US2004034888-A1
                                                                                                                                                                                                                                                                                                                       CAO Y.
                                   Unidentified.
                                                                                                         19-FEB-2004.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              invention
                                                                                                                                                                                                                             (LIUJ/)
(ZHOU/)
(KOVA/)
(SCRE/)
(TABA/)
(CAOY/)
```

NQ Sequence 1628 BP; 412 A; 432 C; 438 G; 346 T; 0 U; 0 Other;

Query Match 53.5%; Score 21.4; DB 13; Length 1628;
Best Local Similarity 80.6%; Pred. No. 93;
Matches 25; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

8 8

Search completed: April 18, 2006, 19:13:04 Job time : 222 secs

```
GenCore version 5.1.7
Copyright (c) 1993 - 2006 Biocceleration Ltd.
```

	Search time 1706.5 Seconds
- nucleic search, using sw model	April 18, 2006, 19:13:18; Search time 1706.5 Seconde
OM nucleic - nu	Run on:

	updates/sec	
(without alignments)	1096.679 Million cell updates/sec	
(without	1096.679	
		SEO3-THEN-SEO4
		T-FORS
		11.

SEQ3-THEN-SEQ4	40	1 agagctgcttggtcagacttatccagattcttggcggtag 40
Title:	Perfect score:	Sednence:

0.1	
TY_NUC 10.0 , Gapext	
: IDENTITY_NUC Gapop 10.0 ,	
oring table	

41078325 segs, 23393541228 residues

Searched:

4000
ţ
Minimum DB cor longth.
Minim

0 2000000000	linimum Match 0% aximum Match 100%
seq length: 0 seq length: 20	ΣΣ
Minimum DB seq 1 Maximum DB seq 1	Post-processing:

March 100% first 45 summaries	1.06 4.07 4.08 -
Maximum Me Listing fi	EST:* 1: 9b est1:* 2: 9b est2:* 3: 9b est2:* 4: 9b est4:* 5: 9b est6:* 7: 9b est6:* 10: 9b est7:* 10: 9b est1:* 11: 9b 983:
	**
	Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	AQ747245 HS 5537 A	AV561271 AV561271	AZ754258 Jhc0001 M	AI993189 701495652	BZ297325 CG3358.rl	T46556 9819 Lambda	BZ293976 CG0632.rl	BZ294269 CG0802.rl	BQ649105 AGENCOURT	CC530433 CH240_406	CC500299 CH240_338	AZ959690 2M0227020	AY105678 Zea mays	DR799776 ZM BFb002	DR798417 ZM_BFb002	AI375672 tc09d09.x	BI192993 602947236	BF037479 601461090	BX104573 BX104573	CC068351 CSU-K33r.	BQ648729 AGENCOURT	BQ668572 AGENCOURT
SUMMARIES	OI.	AQ747245	AV561271	AZ754258	A1993189	BZ297325	T46556	BZ293976	BZ294269	BQ649105	CC530433	CC500299	AZ959690	AY105678	DR799776	DR798417	AI375672	BI192993	BF037479	BX104573	CC068351	BQ648729	BQ668572
	DB	6	Н	6	-	6	œ	0	σ	Ŋ	σ	σ	σ	4	œ	œ	٦	~	8	Ŋ	σ	'n	ß
	Length DB	931	470	501	208	576	581	592	599	954	716	807	610	728	771	829	413	549	675	682	750	942	945
d	Query	61.0	58.0	58.0	58.0	58.0	58.0	58.0	58.0	58.0	57.5	57.5	57.0	57.0	57.0	57.0	56.5	56.5	56.5	56.5	56.5	56.5	56.5
	Score	24.4	23.2	23.2	23.2	23.2	23.2	23.2	23.2	23.2	23	23	22.8	22.8	22.8	22.8	22.6	22.6	22.6	22.6	22.6	22.6	22.6
	Result No.	0 1	7	e	4	'n	φ	7	60	0	c 10	11	c 15	c 13	٦	c 15	16	17	18	19	c 50	21	22

44 rD	B155/640 L355/640 AA144313 mr97h11.r AQ083572 RPCII1-52 BB433173 BB433173 B1086000 2102-21 M	u m u b		AA908125 TENSO967 DT106262 JGI ANNN7 DT110751 JGI ANNO1 BW013500 BW013500 CV120865 AGENCOURT CC142604 NDL.49E24
BG429091 CL328874 CL566935 CX118162	BY357640 AA144313 AQ083572 BB433173	BW358295 BQ828855 CN534408	CB183965 AA958222 AZ927744 BB145092 AI066314	AA908125 DT106262 DT110751 BW013500 CV120865 CC142604
8128	v 4 o 6 u		9 1 6 2 1	188576
976 521 806 814	262 438 520 548	613 620 693	897 284 376 377	543 649 773 801
86.0 86.0 86.0	ນ ນຸດທຸດ ນຸດທຸດ ນຸດທຸດ		55.0 55.0 55.0	55.0 55.0 55.0 50.0
22222 22222 6444	22222	2222	55 55 55 55 55 55 55 55 55	222222
2223	3000	3337	33 33 33 33 33	4 4 4 4 4 0 1 2 2 4 3
U	U U	טטטט	υ υυ	υ

ALIGNMENTS

RESULT 1	
AQ747245/c	
rocus	AQ747245 931 bp DNA linear GSS 19-JUL-1999
DEFINITION	HS_5537_A1_D05_T7A_RPCI-11 Human Male_BAC_Library Homo sapiens cenomic_clone_D1ate=1113_Col=9_Row=G. cenomic_survey_sequence.
NOTOGOODE	NOTATION C.
ACCESSION.	
VERSION	AQ/4/245.1 GI:5554403
NEI WORLS	
SOURCE	Homo sapiens (human)
ORGANISM	
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
	Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhin;
	Hominidae; Homo.
REFERENCE	1 (bases 1 to 931) Mahairas G G Wallace I C Smith K Swartzell S. Holzman T.
4.14.1	nove, u. Gownsonce teamod connectors. A semisare approach to mapping and
	organist the himse deforms
TANGLIOT	DESCRIPTION OF THE DESCRIPTION OF (17) 9739-9744 (1999)
PUBMED	10449764
COMMENT	Contact: Mahairas GG, Wallace JC, Hood L
	High Throughput Sequencing Center
	University of Washington
	401 Queen Anne Avenue North, Seattle, WA 98109, USA
	Tel: (206) 616-3618
	Fax: (206) 616-3887
	Email: jwallace@u.washington.edu
	Clones are derived from the human BAC library RPCI-11. For BAC
	library availability, please contact Pieter de Jong
	(pieter@dejong.med.buffalo.edu). Clones may be purchased from
	BACPAC Resources (http://bacpac.med.buffalo.edu/ordering bac.htm)
	or from Resear h Genetics (info@resgen.com). BAC end Web Server:
	http://www.htsc.washington.edu
	Plate: 1113 row: G column: 9
	Seq primer: T7
	Class: BAC ends
	High quality sequence stop: 931.
FEATURES	Location/Qualitiers
Bource	1
	/organism="Homo Bapiens"
	/mor_cype="genomic Data" /db xref="taxon:9606"
	/clone="Plate=1113 Col=9 Row=G"
	/sex="male"

```
/cell line="RW4"
/lab host="E.coli"
/lab host="E.coli"
/clone_lib="Wouse ES genomic library"
/clone_lib="Wouse ES genomic library"
/note="Vector: peleloBAC11; Site 1: HindIII; Site 2:
HindIII; The mouse ES library was created by ligating
large-size DNA fragments from RW4 cells into the HindIII
cloning site of the pBeloBAC11 vector. The recombinant
vector was then electroporated into DH10B host cells. The
inserts for the library BAC clone are ~120kb and are
flanked in the vector by T? and Sp6 RNA promoters on
either side of the HindIII cloning site. The library was
constructed by Genome Systems (now Incyte). "
                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutheria; Eutheria; Butheria; Buarchontoglires; Glires; Rodentia; Sciurognathi; Muroidea; Murinae; Mus.

1 (Dasse 1 to 501)

2 (hai.J.H., Locke,D.P., Ohta,T., Greally,J.M. and Nicholls,R.D. A cluster of intronless genes in the Prader-Willi syndrome region of mouse chromosome 7C, including a novel imprinted gene, Frat3

Londact: Nicholls RD

Department of Psychiatry, and Department of Genetics
University of Pennsylvania School of Medicine
Room 530, CRB, 415 Curie Blvd, Philadelphia, PA 19104-6140, USA
Tel: 215 898 0273

Email: robertnômail.med.upenn.edu row: 337 column: L11
Seg primer: SP6 sequence primer
Class: BAC ends
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  508 bp mRNA linear EST 08-SEP-1999 CDN4 clone 701495652, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnollophyta; eudicotyledons; core eudicotyledons; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

(chen, J., Moniyama, M., Chan, E., Mooney, M., Carroon, B., Gilliland, D., Wang, X., Hillman, J., Guegler, K., Kim, C., Doyle, M., Brzoska, P., Gorgone, G., Burns, D., Griffin, J., Mouanoutoua, M., Wayren, D., Tan, R., Rose, M., Warren, B., Ton, B., Kastury, K., Borillo, C., Carplo, T., Policky, J., Suzuki, G., Argentine, C., Shah, S., Nobriga, A., Murry, L., Turner, C., Krikorian, S., Elder, L. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Unpublished (1999)
Contact: David Smoller, Ph.D.
Genome Systems, Inc., a wholly owned subsidiary of Incyte
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 501;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Arabidopsis thaliana Gene Expression MicroArray
Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      58.0%; Score 23.2; DB 9; 77.8%; Pred. No. 2.7e+02; iive 0; Mismatches 8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          5 CTGCTTGGTCAGACTTATCCAGATTCTTGGCGGTAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Arabidopsis thaliana (thale cress)
Arabidopsis thaliana
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /organism="Mus musculus"
/mol_type="genomic DNA"
/strain="129/Sv"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              'db xref="taxon:10090"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         clone="337L11"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AI993189.1 GI:5840094
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity 77.8
nes 28; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1. .501
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ROUTCE
  ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TITLE
JOURNAL
COMMENT
                                                                                                                                                                                                                                JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches
                                                                                                                                             AUTHORS
                                                                                                                REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AI993189
                                                                                                                                                                        TITLE
                                                                                                                                                                                                                                                              COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            요
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Varidiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Varidiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; rosids; eurosids II; Brassicates; Brassicaceae; Arabidopsis.

1 (bases 1 to 47). Sato, S. and Tabata, S. A large scale analysis of cDNA in Arabidopsis thaliana: Generation of 12,028 non-redundant expressed sequence tags from normalized and size-selected cDNA libraries
DNA Res. 7 (3), 175-180 (2000)
                       /note="Vector: pBACe3.6; Site_1: EcoRI; Site_2: EcoRI; Male blood DNA was isolated from one randomly chosen donor and partially digested with a combination of EcoRI and EcoRI Methylase. Size selected DNA was cloned into the pBACe3.6 vector at EcoRI sites"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Contact: Erika Agamizu
The First Laboratory for Plant Gene Research
Kazusa DNA Research Institute
Yana 1532-3, Kisarazu, Chiba 292-0812, Japan
Email: asamizu@kazusa.or.jp, URL.http://www.kazusa.or.jp/en/plant/.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           JAC1011 Mouse ES genomic library Mus musculus genomic clone 337L11, genomic survey sequence.
                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AVS61271 Arabidopsis thaliana green siliques Columbia Arabidopsis thaliana green siliques Columbia Arabidopsis thaliana cDNA clone SQ148e10F 3', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /tissue type="green siliques"
/clone lib="Arabidopsis thaliana green siliques Columbia"
/note="Vector: pBluescriptII SK-; Site_1: EcoRI; Site_2:
XhoI"
                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  58.0%; Score 23.2; DB 1; Length 470; 77.8%; Pred. No. 2.6e+02; ive 0; Mismatches 8; Indels
                                                                                                                                                                                                                             DB 9; Length 931;
'clone_lib="RPCI-11 Human Male BAC Library"
                                                                                                                                                                                                                                                                                     6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       . 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         411 AGCTGCAATGTCATACTTATCAGGTTTCTTGGAGGT 446
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /organism="Arabidopsis thaliana"
/mol_type="mRNA"
/ecotype="Columbia"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3 AGCTGCTTGGTCAGACTTATCCAGATTCTTGGCGGT 38
                                                                                                                                                                                                                                                                                                                                                                                 432 CTGCTTGTTCAGATTTATCCACATGCTTGCCAGT 399
                                                                                                                                                                                                                                                                                                                                              5 CIGCITGGICAGACTIAICCAGAIICTIGGCGGI 38
                                                                                                                                                                                                                             th 61.0%; Score 24.4; D
Similarity 82.4%; Pred. No. 99;
28; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Arabidopsis thaliana (thale cress)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           470 bp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /db xref="taxon:3702"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /clone="SQ148e10F"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ā2754258
A2754258.1 GI:12661200
GSS.
Mus musculus (house mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AV561271
AV561271.1 GI:8732697
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity 77.8 Matches 28; Conservative
                                                                                                                                                                                                                                                        Local Similarity
                                                                                                                                                                                                                                Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
```

DEFINITION

RESULT 3 AZ754258

ઠે

ACCESSION

VERSION KEYWORDS SOURCE

KEYWORDS SOURCE ORGANISM

AUTHORS TITLE

REFERENCE

JOURNAL PUBMED COMMENT

FEATURES

DEFINITION

RESULT 2 AV561271

ACCESSION

VERSION

Matches

ö

Gaps

.

Indels

source

ORIGIN

PEATURES

```
Arabidopsis thaliana (thale cress)
Arabidopsis thaliana
Arabidopsis thaliana
Bukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Bukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; cosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
1 (Bases I to 581)
1 (Bases I to 581)
Newman, T., Gebruijn, F., Green, P., Keegstra, K., Kende, H., McIntosh, L., Ohlrogge, J., Raikhel, N., Somerville, S., Thomashow, M., Retzel, E. and Somerville, C.
Genes galore: a summary of methods for accessing results from large-scale partial sequencing of anonymous Arabidopsis cDNA clones Plant. Physiol. 106, 1241-1255 (1994)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BZ293976 1:0073-2002 CG0632.rl Candida glabrata Random Genomic Library Candida glabrata genomic clone CG0632, genomic survey sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /clone_lib=Tranbda-PRL2"
/clone_lib=Tranbda-PRL2"
/note="Vector: lambda Zip-Lox; Site_1: Sal; Site_2: Not;
Lambda PRL2 is a cDNA library derived from equal
quantities of 4 pools of second sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Candida glabrata
Candida glabrata
Candida glabrata
Candida glabrata
Bukaryota; Fungi; Ascomycota; Saccharomycetes;
Saccharomycetales; Candida.
1 (bases 1 to 592)
Wong,S., Pares,M.A., Zimmermann,W., Butler,G. and Wolfe,K.H.
Evidence from comparative genomics for a complete sexual cycle in the 'asexual' pathogenic yeast Candida glabrata
   9819 Lambda-PRL2 Arabidopsis thaliana cDNA clone 135E23T7, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              7846151
On Jan 9, 1998 this sequence version replaced gl:949555.
Contact: Thomas Newman
MSU-DOE Plant Research Laboratory
Michigan State University
MSU-DOB-PEL, Michigan State University, Plant Biology Bldg., E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ch 58.0%; Score 23.2; DB 8; Length 581; 1 Similarity 77.8%; Pred. No. 2.7e+02; 28; Conservative 0; Mismatches 8; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      211 AGCTGCAATGTCATACTTATCAGGTTTCTTGGAGGT 246

    .581
    /organism="Arabidopsis thaliana"

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3 AGCTGCTTGGTCAGACTTATCCAGATTCTTGGCGGT 38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /mol type="RNA"
/ecotype="Columbia"
/db xref="taxon:3702"
/clone="135E23T7"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Tel: 517-353-0854
Fax: 517-353-9168
Email: 22313tcn@ibm.cl.msu.edu
Seq primer: T7 dye primer.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           oligo dT primed cDNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BZ293976
BZ293976.1 GI:24434315
                                                                                                         T46556.1 GI:2763239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GSS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 VERSION
KEYWORDS
SOURCE
ORGANISM
                                                                                                                                                                                                           ORGANISM
   DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 JOURNAL
PUBMED
COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REFERENCE
AUTHORS
TITLE
                                                                                                                                                                                                                                                                                                                                                     REFERENCE
AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches
                                                                        ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ACCESSION
                                                                                                         VERSION
KEYWORDS
SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 7
BZ293976
LOCUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ò
                                                                                                                                                                                                                                                                                                                                                  /clone="701495652"
/clone lib="A. thaliana, Ohio State clone set"
/note="CDNA libzary was made from selected clones from the
Arabidopsis thaliana Ohio State clone set."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BZ297325
CG3358.rl Candida glabrata Random Genomic Library Candida glabrata
genomic clone CG3358, genomic survey sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EST 04-AUG-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Candida glabrata
Candida glabrata
Candida glabrata
Bukaryota, Fungi, Ascomycota, Saccharomycetes,
Bukaryota, Fungi, Ascomycota, Saccharomycetales,
Saccharomycetales, mitosporic Saccharomycetales, Candida.

1 (bases 1 to 576)
Wong, S., Fares, M.A., Zimmermann, W., Butler, G. and Wolfe, K.H.
Bvidence from comparative genomics for a complete sexual cycle in
the 'asexual' pathogenic yeast Candida glabrata
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /organism="Candida glabrata"
/mol_type="genomic DNA"
/strain="CBS 138"
/db_xref="taxon:5478"
/clone="CG3358"
/clone_lib="Candida glabrata Random Genomic Library"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 23.2; DB 9; Length 576;
Pred. No. 2.7e+02;
0; Mismatches 8; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 58.0%; Score 23.2; DB 1; Length 508; Best Local Similarity 77.8%; Pred. No. 2.7e+02; Matches 28; Conservative 0; Mismatches 8; Indels
Pharmaceuticals, Inc.
4633 World Parkway Circle, St. Louis, MO 63134, USA Tel: 877-2733

Pax: 314-427-3324

Email: service@genomesystems.com.
Location/Qualifiers
1. 508
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                211 AGCTGCAATGTCATACTTATCAGGTTTCTTGGAGGT 246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3 AGCTGCTTGGTCAGACTTATCCAGATTCTTGGCGGT 38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Contact: Wong S
Department of Genetics, Smurfit Institute
Trinity College Dublin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CTGCTTGGTCAGACTTATCCAGATTCTTGGCGGTAG 40
                                                                                                                                                                                                                                            /organism="Arabidopsis thaliana"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              581 bp
                                                                                                                                                                                                                                                                             /mol_type="mRNA"
/db_xref="taxon:3702"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BZ297325.1 GI:24439812
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            query Match 58.0%;
Best Local Similarity 77.8%;
Matches 28; Conservative 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Email: swong@tcd.ie
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Class: plasmid ends
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Dublin 2, Ireland
Tel: 353 1 6082319
Fax: 353 1 6798558
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                12620120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              T46556
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           437
```

VERSION KEYWORDS SOURCE ORGANISM

REFERENCE AUTHORS TITLE

JOURNAL

COMMENT

PEATURES

RESULT 6 T46556 LOCUS

ò

DEFINITION

RESULT 5 BZ297325

8

ACCESSION

ö

Gaps

ö

JOURNAL PUBMED

COMMENT

FEATURES

```
/Listue_type="https://listue_type="https://listue_type="https://listue_type="https://listue_type="https://listue_type="https://listue_type="https://listue_type="https://listue_type="https://listue_type="https://listue_type="https://listue_type="https://listue_type="https://listue_type="https://listue_type="https://listue_type="https://listue_type="https://listue_type="https://listue_type="https://listue_type="https://listue_type="https://listue_type="https://listue_type="https://listue_type="https://listue_type="https://listue_type="https://listue_type="https://listue_type="https://listue_type="https://listue_type="https://listue_type="https://listue_type="https://listue_type="https://listue_type="https://listue_type="https://listue_type="https://listue_type="https://listue_type="https://listue_type="https://listue_type="https://listue_type="https://listue_type="https://listue_type="https://listue_type="https://listue_type="https://listue_type="https://listue_type="https://listue_type="https://listue_type="https://listue_type="https://listue_type="https://listue_type="https://listue_type="https://listue_type="https://listue_type="https://listue_type="https://listue_type="https://listue_type="https://listue_type="https://listue_type="https://listue_type="https://listue_type="https://listue_type="https://listue_type="https://listue_type="https://listue_type="https://listue_type="https://listue_type="https://listue_type="https://listue_type="https://listue_type="https://listue_type="https://listue_type="https://listue_type="https://listue_type="https://listue_type="https://listue_type="https://listue_type="https://listue_type="https://listue_type="https://listue_type="https://listue_type="https://listue_type="https://listue_type="https://listue_type="https://listue_type="https://listue_type="https://listue_type="https://listue_type="https://listue_type="https://listue_type="https://listue_type="https://listue_type="https://listue_type="https://listue_type="https://listue_type="https://listue_type="https://listue_t
                                                                                            BQ649105 954 bp mRNA linear BST 15-JUL-2002
AGENCOURT_8188363 NIH_MGC_100 Homo sapiens cDNA clone IMAGE:6283618
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CC530433 17-JUN-2003
CH240_406N8.TARBAC13P2 CHORI-240 Bos taurus genomic clone
CH240_406N8, genomic survey sequence.
                                                                                                                                                                                                                                                                                                                                                       Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Butheria, Buarchontoglires, Primates, Catarrhini;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Butheria, Laurasiatheria, Cetartiodactyla, Ruminantia,
Pecora, Bovidae, Bovinae, Bos.

    (bases 1 to 716)

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Email: cgapbs-remail.nih.gov
Tissue Procurement: CGAP (Stanford)
cDNA Library Preparation: Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MCC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCM2479 row: o column: 11
High quality sequence start: 358
High quality sequence stop: 493.
                                                                                                                                                                                                                                                                                                                                                                                                               Hominidae, Homo.

1 (bases 1 to 954)

NIH-MGC http://mgc.nci.nih.gov/.

Unpublished (1999)

Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           58.0%; Score 23.2; DB 5; Length 954; 77.8%; Pred. No. 3e+02; Live 0; Mismatches 8; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                637 GAGCTGGTGGGCCAGCTCATCCAGATTCTTGGCTG 672
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2 GAGCTGCTTGGTCAGACTTATCCAGATTCTTGGCGG 37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1. 954
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:6283618"
                                                                                                                                                    5', mRNA sequence.
BQ649105.
BQ649105.1 GI:21773277
EST.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CC530433.1 GI:31848721 GSS.
                                                                                                                                                                                                                                                                                        Homo sapiens (human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Library."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             28; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bos taurus (cow)
Bos taurus
                                                                                                                                                                                                                                                                                                                          Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
                                                                                                                                                                                                                                                    KEYWORDS
SOURCE
ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             VERSION
KEYWORDS
SOURCE
ORGANISM
                                                                                                                       DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 10
CC530433/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE
JOURNAL
COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                 REFERENCE
AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches
                                                                                                                                                                                     ACCESSION
                                 RESULT 9
BQ649105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FEATURES
                                                                                                                                                                                                                          VERSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              B2294269 531-OCT-2002 GO802.rl Candida glabrata Random Genomic Library Candida glabrata genomic clone CG0802, genomic survey sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 (bases 1 to 59) Wong. S., Fares, M.A., Zimmermann, W., Butler, G. and Wolfe, K.H. Evidence from comparative genomics for a complete sexual cycle in the 'asexual' pathogenic yeast Candida glabrata Genome Biol. 4 (2), R10 (2003)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Candida glabrata
Candida glabrata
Bukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; mitosporic Saccharomycetales; Candida.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                           /organism="Candida glabrata"
/mol type="genomic DNA"
/strain="CBS 138"
/db xref=traxon:5478"
/clone="CG0632"
/clone_lib="Candida glabrata Random Genomic Library"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /db_xref="taxon:5478"
/clone="CG0802"
/clone_lib="Candida glabrata Random Genomic Library"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 592;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         58.0%; Score 23.2; DB 9; Length 599; 77.8%; Pred. No. 2.7e+02; ive 0; Mismatches 8; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        8; Indels
                                                 Contact: Wong S
Department of Genetics, Smurfit Institute
Trinity College Dublin
Dublin 2, Ireland
Tel: 353 1 608219
Fax: 353 1 679858
Email: swong@tcd.ie
Class: plasmid ends.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        437 CTGGATGTTGTAACTTATCTAGATTCTTTGCGGTAG 472
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               437 CTGGATGTTGTAACTTATCTAGATTCTTTGCGGTAG 472
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Contact: Wong S
Department of Genetics, Smurfit Institute
Trinity College Dublin
Dublin 2, Ireland
Trel: 353 1 6082319
Fax: 353 1 679858
Email: swong@tcd.ie
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ch 58.0%; Score 23.2; DB 9; 1. Similarity 77.8%; Pred. No. 2.7e+02; 28; Conservative 0; Mismatches 8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    5 CTGCTTGGTCAGACTTATCCAGATTCTTGGCGGTAG 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          5 CTGCTTGGTCAGACTTATCCAGATTCTTGGCGGTAG 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /organism="Candida glabrata"
/mol_type="genomic DNA"
/strain="CBS 138"
Genome Biol. 4 (2), R10 (2003)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BZ294269
BZ294269.1 GI:24434793
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Class: plasmid ends
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                       1. .592
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity
Matches 28; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                12620120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      KEYWORDS
SOURCE
ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              source
```

DEFINITION

RESULT 8 BZ294269

쉱

Matches

ORIGIN

ACCESSION VERSION

REFERENCE AUTHORS TITLE

JOURNAL PUBMED COMMENT

FEATURES

ORIGIN

g ઠે

ö

Gaps

ö

seq3-then-seq4.rst

TITLE JOURNAL COMMENT

AUTHORS

```
Sequencing
The British Columbia Cancer Agency Genome Science Centre
600 W. 10th Ave, Vancouver, British Columbia, Canada V52 4E6
711 604-877-6085
Fax: 604-877-6276
Bmail: rholt@bcgsc.ca
Clones are derived from the bovine BAC library CHORI-240
(http://www.chori.org/bacpac/bovine240.htm). For BAC library
availability, please contact Pieter de Jong (pdejong@mail.cho.org).
Clones may be purchased from BACPAC Resources
(http://www.chori.org/bacpac/ordering information.htm). This work
was undertaken as part of the International Bovine BAC Mapping
Consortium (IBBMC) by CSIRO Livestock Industries, Australia and the
British Columbia Genome Sciences Centre, Canada.
Seq primer: SP6
Class: BAC ends.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AZ959690 10xb plasmid UUGC2M library Mus musculus genomic clone UUGC2M0227020 P, genomic survey sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Buarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /cell_type="Blood"
/clone_lib="CHORI-240"
/note="Wector: pTARBAC1.3; Site_1: Mbol; Site_2: Mbol;
Hereford bull Li Domino 99375; CHORI-240 Bovine BAC
library (Male) produced by Pieter de Jong"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 (bases 1 to 610)
1 (bases 1 to 610)
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R. Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
Unpublished (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 57.5%; Score 23; DB 9; Length 807; 83.9%; Pred. No. 3.5e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Std Error: 0.00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 657 AGAGCTGCTTGTTCAGATTTGTCCAGAGCCT 687
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 AGAGCTGCTTGGTCAGACTTATCCAGATTCT 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /mol_type="genomic DNA"
/strain="breed: Hereford"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /organism="Bos taurus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunm@genetics.utah.edu
Insert Length: 10000 Std Brro
Plate: 0227 row: O column: 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /db_xref="taxon:9913"
/clone="CH240_33811"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mus musculus (house mouse)
Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AZ959690.1 GI:13830917
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /sex="Male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             26; Conservative
                Contact: Rob Holt
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           84112,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GSS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 12
AZ959690/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  VERSION
KEYWORDS
SOURCE
ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ઠે
                                                                                                                                                                                                                                                                                                                                                    Sequencing
The British Columbia Cancer Agency Genome Science Centre
600 W. 10th Ave, Vancouver, British Columbia, Canada V52 4E6
601 W. 10th Ave, Vancouver, British Columbia, Canada V52 4E6
Fax: 604-877-6085
Fax: 604-877-6276
Email: rholt@bcgsc.ca
Clones are derived from the bovine BAC library CHORI-240
(http://www.chori.org/Dacpac/bovine240.htm). For BAC library
availability, please contact Pieter de Jong (pdejong@mail.cho.org).
Clones may be purchased from BACPAC Resources
(http://www.chori.org/bacpac/ordering information.htm). This work
was undertaken as part of the International Bovine BAC Mapping
Consortium (IBBMC) by CSIRO Livestock Industries, Australia and the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CC500299 807 bp DNA linear GSS 17-JUN-2003
CH240_33811.TARBAC13P2 CHORI-240 Bos taurus genomic clone
CH240_33811, genomic survey sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae; Bovinae; Bos. 1 (bases 1 to 807). To the to the to the top to the top the 
Holt, R., Stott, J., Yang, G., Barber, S., Smailus, D., Prabhu, A.-L., Tsai, M., Cloutier, A., Lee, D., Girn, N., Olson, T., Mayo, M., Butterfield, Y., Kirkpatrick, R., Liu, J., Guin, R., Chan, A., Chiu, R., Schein, J., Marra, M., de Jong, P., Brown-John, M., Jones, S., Schein, J., Marra, M., de Jong, P., Keele, J. W. and Kappes, S.M. Bovine BAC End Sequences from Library CHORI-240, PLATES 399 to 478 Unpublished (2003)
Contact: Rob Holt
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /cell type="Blood"
/clone_lib="CHORI-240"
/note="Vector: pTARBACL.3; Site_1: MboI; Site_2: MboI;
Hereford bull il Domino 99375; CHORI-240 Bovine BAC
library (Male) produced by Pieter de Jong"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 716;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             57.5%; Score 23; DB 9; I
83.9%; Pred. No. 3.4e+02;
tive 0; Mismatches 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 AGAGCTGCTTGGTCAGACTTATCCAGATTCT 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /organism="Bos taurus"
/mol_type="genomic DNA"
/strain="breed: Hereford"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /db_xref="taxon:9913"
/clone="CH240_406N8"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Plate: 406 row: N column: 8
Seg primer: SP6
Class: BAC ends.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Location/Qualifiers
1. .716
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Unpublished (2003)
Other_GSSs: CH240_338I1.T7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CC500299.1 GI:31818551
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /sex="Male
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity 83.9
Matches 26; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bos taurus (cow)
Bos taurus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
```

source

PEATURES

ACCESSION VERSION KEYWORDS SOURCE ORGANISM

REFERENCE

TITLE JOURNAL COMMENT

DEFINITION

RESULT 11 CC500299

DRIGIN

ö

Gaps ö GSS 27-APR-2001

```
DR799776
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 14
DR799776/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ORGANISM
  TITLE
JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TITLE
JOURNAL
COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    VERSION
KEYWORDS
SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REFERENCE
                                                                                                                                                                                                                                            FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FEATURES
                                                                        COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LOCUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          g
                                                                                                                                                                                                                                                                                                                                                                             (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polymuclectide kinase. Adaptor oligonuclectides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gelectrophoresis. Vector DNA was prepared from a derivative of pWAPA2 (gil 4732114 [gb] AR125072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli X110-Gold (Stratagene) cells and selected for ampicillin resistance."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HTC 22-FEB-2005
                                                                                                                                                                                                                                                           /lab_host="E. coli strain XLIO-Gold, T1-resistant, F-"
/clone lib="Mouse 10kb plasmid UUGCZM library"
hoto="Vector: PWD42nv; Purified genomic DNA from M.
musculus G57BL/GJ (female) was obtained from the Jackson
Laboratory Mouse DNA Resource
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae, PACCAD
clade, Panicoldeae, Andropogoneae, Zea.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gardiner, J., Schroeder, S., Polacco, M.L., Sanchez-Villeda, H., Fang, Z., Morgante, M., Landewe, T., Fengler, K., Useche, F., Hanafey, M., Tingey, S., Chou, H., Wing, R., Soderlund, C. and Coe, E.H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Anchoring 9,371 maize expressed sequence tagged unigenes to the bacterial artificial chromosome contig map by two-dimensional overgo hybridization
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Hainey, C.F., Dolan, M., Miao, G.H., Vogel, J.M., Whitsitt, M.S., Arthur, L.W., Hanafey, M., Morgante, M. and Tingey, S.V. Maize Mapping Project/DuPont Consensus Sequences for Design of Overgo Probes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 22.8; DB 9; Length 610;
Pred. No. 4e+02;
0; Mismatches 7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    474 AGAGTTTCTAGGTCAGACTTCTACAGGTTCTTTG 441
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Plant Physiol. 134 (4), 1317-1326 (2004)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AGAGCTGCTTGGTCAGACTTATCCAGATTCTTGG 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            mRNA
Seg primer: CGTTGTAAAACGACGGCCAGT
Class: plasmid ends
High quality sequence stop: 610.
Location/Qualifiers
                                                                                                                  /organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AY105678 728 bp
Zea mays PC0138313 mRNA sequence.
AY105678
                                                                                                                                                                                          /db_xref="taxon:10090"
/clone="UUGC2M0227020"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AY105678.1 GI:21208756
                                                                                                                                                                                                                                            /sex="Female"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ch 57.0%;
1 Similarity 79.4%;
27; Conservative 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (bases 1 to 728)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (bases 1 to 728)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (bases 1 to 728)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Overgo Probes
Unpublished (2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
Matches 27; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Zea шаув
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Zea mays
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Coe, E.H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DEFINITION
ACCESSION
VERSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     KEYWORDS
SOURCE
ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 13
AY105678/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REFERENCE
AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PUBMED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REFERENCE
                                                                     FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DRIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  셤
```

```
Direct Submission
Submitted (25-APR-2002) Maize Mapping Project, University of
Missouri, Columbia, MO 65211, USA
Missouri, Columbia, MO 65211, USA
If you are interested in getting corresponding physical clones,
these are publicly available from ZmDB and may be found by BLAST
searching at MSL, maizemap.org; ZmDB, www.zmdb.iastate.edu; TIGR,
www.tigr.org; or NCBI, www.ncbi.nlm.nih.gov. When the source of the
schable, Iowa State, then clones may be requested from ZmDB:
www.zmdb.iastate.edu.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EST 27-JUL-2005
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae, PACCAD
clade, Panicoideae, Andropogoneae, Zea.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Kim,H., Collura,K., Wissotski,M., Smart,D., Kudrna,D., Muller,C., Rao,K., Haller,K., Wing,R., Soderlund,C., Walbot,V. and Yu,Y. Maize Full-length cDNA Project Unpublished (2005)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note="this sequence is part of a project of EST assemblies resulting from the application of public contigs to seed DuPont contigs; this resource was assembled by DuPont as part of a collaboration for the overgo addressing of BACs in conjunction with the Maize Mapping Project"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             db_xref="taxon:4577"
/db_xref="taxon:4577"
/tissue_type="mixed (sliks, husks, ears, pollen, shoot
/tissue_type="mixed (sliks, whole seed, embryo)"
/dev_stage="varies by tissue"
/lab_host="varies by tissue"
/lab_host="Tax BRb"
/clone_lib="zw_BRb"
/note="Vector: pcMV-SPORT_6.1; Site_1: EcoRV; Site_2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note="Vector:"pCMV-SPORT 6.1; Site 1: EcoRV; Site 2: Not1; Maize Full length cDNA library (3530 library)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /mol_type="mRNA" //mol_type="mRNA" //mol_type="mRNA" //db_xref="MaizeGDB:638121" //db_xref="taxon:4577" //db_xref=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                771 bp mRNA linear EST
BFb0022N18.r ZM_BFb Zea mays cDNA 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 57.0%; Score 22.8; DB 4; Length 728; Best Local Similarity 79.4%; Pred. No. 4.18+02; Matches 27; Conservative 0; Mismatches 7; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Contact: Yelsoo Yu
Arizona Genomics Institute
The University of Arizona
Forbes Bullding Room 303, Tucson, AZ 85721-0036, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                305 GCAGCTIGGTCAGACTGTTCATGTTTCTTGGAGG 272
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               4 GCTGCTTGGTCAGACTTATCCAGATTCTTGGCGG 37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Email: yeisoo@genome.arizona.edu
Plate: 0022 row: N column: 18.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /organism="Zea mays"
/mol_type="mRNA"
/cultivar="B73"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /organism="Zea mays"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DR799776.1 GI:71326170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Tel: 520 626 9585
Fax: 520 621 1259
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ZM BFb002
DR799776
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Zea mays
Zea mays
```

```
created by Invitrogen from multiple tissues; Organ: silks, husks, ears, pollen, shoot tips, leaf, root tips, whole seed, embryo. This is a Gateway compatible vector, permitting clone movement to new vector backbones for expression in diverse host cells using recombination rather than restriction enzymes. poly(A)+ mRNA was prepared by Invitrogen, and equimolar amounts of RNA from each of the 12 tissue samples were mixed together for selection of mRNA with a 5' cap. After synthesis of cDNA, a normalization step was conducted against the mixture of RNA sources. Tissues prepared: 1, just emerging silks; 2. inner husks from ears of sample #1; 3. 20 dap aleurone; 4. immature tasseals, srages from 1-2 mm to 1-2 cm; 5. 2 mm to 2 cm ears; 6. pollen; 7. 1 cm vegetative shoot tips from 15 day old seedlings; all leaves with an expanded or partially expanded sheath were removed; 8. mature leaf tissue; 9. 0.5 cm long root tips from 15 day old seedlings; 10. 10 dap whole seed; 11. 12 dap endosperm and embryo; 12. 17 dap endosperm and embryo; 12. 17 dap endosperm and embryo; All of the seedlings; inliversity of Arizona. Clones, high density filters and amplified library can be ordered from the University of Arizona.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ch 57.0%; Score 22.8; DB 8; Length 771; 1 Similarity 79.4%; Pred. No. 4.1e+02; 27; Conservative 0; Mismatches 7; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (http://www.genome.arizona.edu/orders/)."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
```

298 GCAGCTIGGICAGACTGTTCATGTTTCTTGGAGG 265 4 GCTGCTTGGTCAGACTTATCCAGATTCTTGGCGG 37 Matches 윱 ò

ORIGIN

рктув417 ZM BFb0020021.r ZM_BFb Zea mays cDNA 5', mRNA sequence. DR798417 DR798417.1 GI:71323512 Zea mays EST RESULT 15 DR798417/c LOCUS DEFINITION ACCESSION VERSION ORGANISM KEYWORDS SOURCE

Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta, Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae, PACCAD clade, Panicoideae, Andropogoneae, Zea.

1 (bases 1 to 829)

1 (Ann.H., Collura, K., Wissotski, M., Smart, D., Kudrna, D., Muller, C., Rao, K., Haller, K., Wing, R., Soderlund, C., Walbot, V. and Yu, Y.

Naize Full-length cDNA Project
Unpublished (2005) REFERENCE AUTHORS

TITLE JOURNAL COMMENT

Arizona Genomics Institute
The University of Arizona
Forbes Building Room 303, Tucson, AZ 85721-0036, USA
Tel: 520 626 9585
Fax: 520 621 1259 Contact: Yeisoo Yu

Bmail: yeisoo@genome.arizona.edu
Plate: 0020 row: O column: 21.
Location/Qualifiers source PEATURES

db_xref="raxon:4577"
/db_xref="raxon:4577"
/tissue type="mixed (silks, husks, ears, pollen, shoot /tissue type="mixed (silks, husks, ears, pollen, shoot /dev_stage="varies by tissue"
/lab_host="bard by tissue"
/lab_host="pollen"
/clone lib="zm_Brb"
/note="vector: pollen"
/note="vector: pollen" /organism="Zea mays" /mol_type="mRNA" /cultivar="B73"

/note="Vector:"pCMV-SPORT 6.1; Site 1: BcoRV; Site 2: Not1; Maize Full length cDNA library (3530 library)

created by Invitrogen from multiple tissues; Organ: silks, husks, ears, pollen, shoot tips, leaf root tips, whole seed, embryo. This is a Gateway compatible vector, permitting clone movement to new vector backbones for expression in diverse host cells using recombination rather than restriction enzymes. poly(A)+ mRNA was prepared by Invitrogen, and equimolar amounts of RNA from each of the 12 tissues samples were mixed together for selection of mRNA with a 5' cap. After synthesis of CDNA, a normalization step was conducted against the mixture of RNA sources. Tissues prepared: 1, just emerging silks; 2. inner husks from ears of sample #1; 3. 20 dap aleurone; 4. inner husks from ears of sample #1; 3. 20 dap aleurone; 4. inner husks from ears of sample #1; 3. 20 dap aleurone; 4. inner husks from ears of sample #1; 3. 20 dap aleurone; 4. inner husks from ears of sample #1; 3. 20 dap aleurone; 4. inner husks from ears of sample #1; 3. 20 dap aleurone; 4. inner husks from ears of sample #1; 3. 20 dap aleurone; 4. inner husks from 15 day old seedlings; 11. 1 can vegetative shoot tips from partially expanded sheath were removed; 8. mature leaf tissue; 9. 0.5 cm long root tips from 15 day old seedlings; 10. 10 dap whole seed; 11. 12 dap endosperm and embryo; 12. 17 dap endosperm and embryo. All of the seedlings; 10. 10 dap whole seed; 11. 12 dap endosperm and ensity filters and amplified library can be ordered from the University of Arizona. Clones, high density filters and amplified library can be ordered from the University of Arizona. (http://www.genome.arizona.edu/orders/)."

ORIGIN

Gaps . 0 Length 829; Indels Score 22.8; DB 8; Pred. No. 4.2e+02; 0; Mismatches 7; Query Match
Best Local Similarity 79.4%;
Matches 27; Conservative

ö

290 GCAGCTTGGTCAGACTGTTCATGTTTCTTGGAGG 257 4 GCTGCTTGGTCAGACTTATCCAGATTCTTGGCGG 37 ŝ 셤

Search completed: April 18, 2006, 20:10:26 Job time : 1710.5 secs

inis Page Blank (uspto)

```
Sequence 866, App
Sequence 14381, A
Sequence 4, Appli
Sequence 7, Appli
Sequence 7, Appli
Sequence 167503,
Sequence 16464, A
Sequence 16464, A
Sequence 12760, A
Sequence 13611, A
Sequence 13611, A
Sequence 1, Appli
Sequence 1, Appli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 15, Appl
Sequence 6434, Ap
Sequence 7, Appli
Sequence 27, Appl
Sequence 27, Appl
Sequence 3, Appli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 15371, A
Sequence 15372, A
Sequence 11804, A
Sequence 1, Appli
                                                          April 18, 2006, 19:28:37; Search time 73.5 Seconds (without alignments) 967.380 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                           Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Description
GenCore version 5.1.7
Copyright (c) 1993 - 2006 Biocceleration Ltd.
                                                                                                                          1 agagctgcttggtcagacttatccagattcttggcggtag 40
                                                                                                                                                                                                                                                                                            Issued Patents NA:*

1: /cgn2 6/ptodata/1/ina/1_COMB.seq:*

2: /cgn2 6/ptodata/1/ina/5_COMB.seq:*

3: /cgn2 6/ptodata/1/ina/6A_COMB.seq:*

4: /cgn2 6/ptodata/1/ina/B_COMB.seq:*

5: /cgn2 6/ptodata/1/ina/H_COMB.seq:*

6: /cgn2 6/ptodata/1/ina/P_COMB.seq:*

7: /cgn2 6/ptodata/1/ina/P_COMB.seq:*

7: /cgn2 6/ptodata/1/ina/P_COMB.seq:*

9: /cgn2 6/ptodata/1/ina/RE_COMB.seq:*

9: /cgn2 6/ptodata/1/ina/RE_COMB.seq:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Total number of hits satisfying chosen parameters:
                                                                                                                                                                           1303057 segs, 888780828 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                       SUMMARIES
                                                                                                                                                                                                                                                    Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                         - nucleic search, using sw model
                                                                                                                                             IDBNTITY NUC
Gapop 10.0 , Gapext 0.1
                                                                                                                                                                                                                     Minimum DB seq length: 0
Maximum DB seq length: 200000000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query
Match Length DB
                                                                                                  SEQ3-THEN-SEQ4
40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       56.5 304533
56.5 304533
56.0 67479
55.5 1600
54.0 254405
53.0 282
53.0 282
53.0 282
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   58133
96074
110000
2181
2181
2181
2181
683
2337
2337
20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       .............
                                                                                                     Title:
Perfect score:
Sequence:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Scoring table:
                                         OM nucleic
                                                                                                                                                                                                                                                                                               Database :
                                                                                                                                                                             Searched:
                                                              Run on:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           00000 0000000
```

Appli Appli Appli Appli 17, Ap 17, Ap 106, A 106, A 1335, Appl Appl Appl Appl Appl Appl Appl App	THEREOF	°°	THEREOF
1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1	USES	Gaрв	USES
sednence sed	OCIATED DETECTION AND USES	4533;	A AND
\$	WED SCTIO	30	NTED
		Length Indel: 7 54978	ASSOCIATED OF DETECTION AND
		n n	ABS AS
55540-14 55540-	NTS WN GENES METHODS 6	22.6; DB 3 No. 19; Ematches GATTCTTGGGG	WN GENES METHODS
9938 9938 9949	NME 6 6	re 22.6; d. No. 19 Mismatche CAGATICTT	
US-09-938-642-4 US-09-938-540-3 US-09-938-540-1 US-09-107-532A-216 US-09-107-532A-216 US-09-949-016-77105 US-09-949-016-77105 US-09-949-016-77105 US-09-949-016-728334 US-09-949-016-128335 US-09-134-010-2572 US-09-134-010-2572 US-09-134-010-2572 US-09-134-010-2572 US-09-134-010-2572 US-09-134-010-2572 US-09-134-010-2572 US-09-134-010-2572 US-09-134-010-2573	ALIG 0994901 al. SMS IN : N DISEA 109/949 14,755 37,768 31,498 or G	56.5%; Score 75.7%; Pred. Live 0; Mis GTCAGACTTATCCAG	US/0994901 g et al. RPHISMS IN
~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~	ation US/09  Craig et a OLYMORPHISM 307TH HUMAN 307TH HUMAN 307TH HUMAN 00-0-0-0-1-14 BER: 60/237 00-10-20 BER: 60/237 00-09-08 207012 Windows Ve	.5%; .7%; e AGACT 	n US/ 1g et ORPHI HUMA
20 20 20 20 20 258 601 601 601 1725 11725 11725 11725 11725 11725 11725 11725 11725 11725 11725 11725 11725 11725 11725 11725 11725 11725 11725 11725 11725 11725 11725 11725 11725 11725 11725 11725 11725 11725 11725 11725 11725 11725 11725 11725 11725 11725 11725 11725 11725 11725 11725 11725 11725 11725 11725 11725 11725 11725 11725 11725 11725 11725 11725 11725 11725 11725 11725 11725 11725 11725 11725 11725 11725 11725 11725 11725 11725 11725 11725 11725 11725 11725 11725 11725 11725 11725 11725 11725 11725 11725 11725 11725 11725 11725 11725 11725 11725 11725 11725 11725 11725 11725 11725 11725 11725 11725 11725 11725 11725 11725 11725 11725 11725 11725 11725 11725 11725 11725 11725 11725 11725 11725 11725 11725 11725 11725 11725 11725 11725 11725 11725 11725 11725 11725 11725 11725 11725 11725 11725 11725 11725 11725 11725 11725 11725 11725 11725 11725 11725 11725 11725 11725 11725 11725 11725 11725 11725 11725 11725 11725 11725 11725 11725 11725 11725 11725 11725 11725 11725 11725 11725 11725 11725 11725 11725 11725 11725 11725 11725 11725 11725 11725 11725 11725 11725 11725 11725 11725 11725 11725 11725 11725 11725 11725 11725 11725 11725 11725 11725 11725 11725 11725 11725 11725 11725 11725 11725 11725 11725 11725 11725 11725 11725 11725 11725 11725 11725 11725 11725 11725 11725 11725 11725 11725 11725 11725 11725 11725 11725 11725 11725 11725 11725 11725 11725 11725 11725 11725 11725 11725 11725 11725 11725 11725 11725 11725 11725 11725 11725 11725 11725 11725 11725 11725 11725 11725 11725 11725 11725 11725 11725 11725 11725 11725 11725 11725 11725 11725 11725 11725 11725 11725 11725 11725 11725 11725 11725 11725 11725 11725 11725 11725 11725 11725 11725 11725 11725 11725 11725 11725 11725 11725 11725 11725 11725 11725 11725 11725 11725 11725 11725 11725 11725 11725 11725 11725 11725 11725 11725 11725 11725 11725 11725 11725 11725 11725 11725 11725 11725 11725 11725 11725 11725 11725 11725 11725 11725 11725 11725 11725 11725 11725 11725 11725 11725 11725 11725 11725 11725 11725 11725 11725 11725 11725	ot George	imilarity 75.7%; Score 22.6; DB 3 imilarity 75.7%; Pred. No. 19; ; Conservative 0; Mismatches AGAGCTGCTTGGTCAGACTTATCCAGATTCTTGGCGG	RESULT 2 US-09-949-016-15372/c ; Sequence 15372, Application US/09949016 ; Patent No. 6812339 ; GENERAL INFORMATION: APPLICANT: VENTER, J. Craig et al. TITLE OF INVENTION: POLYMORPHISMS IN KNO; TITLE OP INVENTION: WITH HUMAN DISEASE, ; FILE REFERENCE: CL001307
	71/c Applic Applic Applic TION:	milarity Conserva GAGCTGCTTG GAGCTTCTTG	6-15372/c 5372, Appl. 6812339 100000000000000000000000000000000000
N N N N N A A A A A A A A A A A A A A A	16-15371/6 16371, App 16371, App 16812339 16812339 1787100 1787100 1787100 1787100 1787100 1787100 1787100 1787100 1787100 1787100 1787100 1787100 1787100 1787100 1787100 1787100 1787100 1787100 1787100 1787100 1787100 1787100 1787100 1787100 1787100 1787100 1787100 1787100 1787100 1787100 1787100 1787100 1787100 1787100 1787100 1787100 1787100 1787100 1787100 1787100 1787100 1787100 1787100 1787100 1787100 1787100 1787100 1787100 1787100 1787100 1787100 1787100 1787100 1787100 1787100 1787100 1787100 1787100 1787100 1787100 1787100 1787100 1787100 1787100 1787100 1787100 1787100 1787100 1787100 1787100 1787100 1787100 1787100 1787100 1787100 1787100 1787100 1787100 1787100 1787100 1787100 1787100 1787100 1787100 1787100 1787100 1787100 1787100 1787100 1787100 1787100 1787100 1787100 1787100 1787100 1787100 1787100 1787100 1787100 1787100 1787100 1787100 1787100 1787100 1787100 1787100 1787100 1787100 1787100 1787100 1787100 1787100 1787100 1787100 1787100 1787100 1787100 1787100 1787100 1787100 1787100 1787100 1787100 1787100 1787100 1787100 1787100 1787100 1787100 1787100 1787100 1787100 1787100 1787100 1787100 1787100 1787100 1787100 1787100 1787100 1787100 1787100 1787100 1787100 1787100 1787100 1787100 1787100 1787100 1787100 1787100 1787100 1787100 1787100 1787100 1787100 1787100 1787100 1787100 1787100 1787100 1787100 1787100 1787100 1787100 1787100 1787100 1787100 1787100 1787100 1787100 1787100 1787100 1787100 1787100 1787100 1787100 1787100 1787100 1787100 1787100 1787100 1787100 1787100 1787100 1787100 1787100 1787100 1787100 1787100 1787100 1787100 1787100 1787100 1787100 1787100 1787100 1787100 1787100 1787100 1787100 1787100 1787100 1787100 1787100 1787100 1787100 1787100 1787100 1787100 1787100 1787100 1787100 1787100 1787100 1787100 1787100 1787100 1787100 1787100 1787100 1787100 1787100 1787100 1787100 1787100 1787100 1787100 1787100 1787100 1787100 1787100 1787100 1787100 1787100 1787100 1787100 1787100 1787100 1787100 1787100 1787100 1787100 1787100 1787100 1787100 1787100 1787100 1787100 178	Simil 8, C AGAG      AGAG	1537, 72, 8123, 8123 8881 8881 VENT VENT VENT
	-016- 016- 016- 016- 016- 016- 016- 016-	atch 3al 2 1 1 5014	9-016-1537; ice 15372; in No. 68123; in No.
2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2	RESULT 1  US-09-949-016-15371/c Sequence 15311, Appl Patent No. 6812339 GENERAL INFORMATION: TITLE OF INVENTION: THORER OF SEQ ID NO. SOFTWARE: FRATURE: TYPE: DNA ORGANISM: Human ORGANISM: HUMAN ORGANISM: HUMAN ORGANISM: HUMAN ORGANISM: HUMAN OFFICE OFFI TITLE TITLE OFFI TITLE T	្ត្រីដូម្លី 🖰	ULT 2 09-949-016-15372/c dequence 15372, App atent No. 6812339 anenal INFORMATION APPLICANT: VENTER, TITLE OF INVENTION TITLE OF INVENTION
00 00 00	RESULT  US-09- US-08- S-09- CORP  TITT  TITT  TITT  TITT  TITT  TITT  PRII  PRII  PRII  PRII  PRII  TY  TY  TY  TY  TY  TY  TY  TY  TY	, ,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,	RESULT US-09- ; Sequ ; Pate ; GENE ; TIT ; TIT
	•	T	

```
; TYPE: DNA
; ORGANISM: Acinetobacter baumannii
US-09-328-352-866
                                                                                                                                                                                                                                                      FEATURE:

NAME/KEY: CDS
LOCATION: (225)..(1388)

OTHER INFORMATION: ccpAl-Gen
US-09-938-540-1
                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 88.9
Matches 24; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best Local Similarity 75.0 Matches 27; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-09-328-352-866/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 6
US-09-949-016-14381
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ઠ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 11804, Application US/09949016
| Batent No. 6812339 | Batent No. 6812339 |
| GENERAL INFORMATION: |
| TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED |
| TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF |
| TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF |
| TITLE REPERENCE: CLOO1307 |
| TITLE REPERENCE: CLOO1307 |
| TITLE REPERENCE: CLOO1307 |
| PRIOR APPLICATION NUMBER: G0/241,755 |
| PRIOR PLIING DATE: 2000-10-20 |
| PRIOR PLIING DATE: 2000-10-03 |
| PRIOR FILING DATE: 2000-10-03 |
| PRIOR FILING DATE: 2000-09-08 |
| NUMBER OF SEQ ID NOS: 207012 |
| SOFTWARE: FREESEQ for Windows Version 4.0 |
| SEQ ID NO 11804 |
| LENGTH: G7479 |
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 3; Length 304533;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 3; Length 67479;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              9; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            14550 AGAGCTGTTTGGTCAGGCTTCTGGCCATCCTTCTGGGTAG 14511
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                255014 AGAGCTTCTTGTTCCGTCTGAGCCAGATCCTTGTTGG 254978
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 AGAGCTGCTTGGTCAGACTTATCCAGATTCTTGGCGGTAG 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 56.5%; Score 22.6; D
Best Local Similarity 75.7%; Pred. No. 19;
Matches 28; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 56.0%; Score 22.4; D
Best Local Similarity 72.5%; Pred. No. 15;
Matches 29; Conservative 0; Mismatches
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR PLING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,496
PRIOR APPLICATION NUMBER: 60/231,496
PRIOR PILING DATE: 2000-10-03
PRIOR PILING DATE: 2000-09-08
SOUTHARE: PASELSEQ FOR WINDOWS VERSION 4.0
SOUTHARE: PASELSEQ FOR WINDOWS VERSION 4.0
SERVITH: 304533
                                                                                                                                                                                                                                                                                                                                                                               NAME/KEY: misc_feature

// LCCATION: (1)...(304533)

// OTHER INFORMATION: n = A,T,C or G

US-09-949-016-15372
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LOCATION: (1)...(67479)
OTHER INFORMATION: n = A,T,C or G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 1, Application US/09938540; Patent No. 6838267; General INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME/KEY: misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 3
US-09-949-016-11804/c
                                                                                                                                                                                                                                                                                                                                   ORGANISM: Human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ORGANISM: Human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-09-949-016-11804
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 4
US-09-938-540-1/c
                                                                                                                                                                                                                                                                                                            TYPE: DNA
```

ઠે

g

ઠ

```
Sequence 866, Application US/09328352
Sequence 866, Application US/09328352
Patent No. 6562958
GENERAL INFORMATION:
APPLICANT: Gary L. Breton et al.
APPLICANT: Gary L. Breton et al.
TITLE OF INVENTION: BAUMANNI FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: BAUMANNI FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: GTC99-03PA
CURRENT APPLICATION NUMBER: US/09/328,352
CURRENT PILING DATE: 1999-16-04
NUMBER OF SEQ ID NOS: 8252
SEQ ID NOS: 8252
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         JOSTON SECURIOR APPLICATION US/09949016

JEACHER NO. 6812339

JETLE PROFESSEL INFORMATION:

JETLE PEPERSMENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

JETLE PEPERSMENT: CLOOL 10307

CURRENT APPLICATION NUMBER: US/09/949, 016

CURRENT PILING DATE: 2000-04-14

PRIOR PILING DATE: 2000-10-20

PRIOR PILING DATE: 2000-10-03

PRIOR PILING DATE: 2000-10-03

PRIOR APPLICATION NUMBER: 60/237, 768

PRIOR PILING DATE: 2000-10-03

NUMBER OF SEC ID NOS: 207012

SOFTHARE: PRESENCE TOWN WINDOWS VERSION 4.0

SEQ ID NO 14381

LENGTH: 254405
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
TITLE OF INVENTION: New nucleotide sequences which code for the ccpAl gene FILE REFRENCE: 000059 BT
CURRENT APPLICATION NUMBER: US/09/938,540
CURRENT FILING DATE: 2001-08-27
NUMBER OF SEQ ID NOS: 4
SOFTWARE: PATENTIN Ver. 2.1
LENGTH.: 1600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 1600;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 3; Length 885;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           260 GCTTCACGTCAGACACATCAAGCTTTTTGGTGGTA 225
                                                                                                                                                                                                                                                                                                                                                                                                                                                         55.5%; Score 22.2; DB 3;
88.9%; Pred. No. 6.5;
tive 0; Mismatches 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4 GCTGCTTGGTCAGACTTATCCAGATTCTTGGCGGTA 39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             54.0%; Score 21.6; I 75.0%; Pred. No. 10; iive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      985 ccercararccacarrerrecectae 959
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              14 CAGACTTATCCAGATTCTTGGCGGTAG 40
                                                                                                                                                                                                                                 TYPE: DNA Orynebacterium glutamicum
```

```
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ANTI-SENSE: NO ORIGINAL SOURCE
                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                              Gaps
                                                                                                                                                                                             Sequence 4, Application US/08440725A

Sequence 4, Application US/08440725A

Patent No. 5985822

GENERAL INFORMATION:
APPLICANT: Rediman, Gerald M.
APPLICANT: Crossin, Kathryn L.
APPLICANT: Sporns, Olaf
ITILE OF INVENTION: INHIBITION OF GLIAL CELL PROLIFERATION
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: THE SCRIPPS RESEARCH INSTITUTE
STREET: 10550 No. 5985822th Torrey Pines Road, TPC-8
CITY: La Jolla
STARE: California
                                                             Score 21.6; DB 3; Length 254405; Pred. No. 50;
                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 2; Length 282;
                                                                                              9; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                              241977 GIGCIGCITGGITAGAATITIGAAGAITCTICTCAG 242012
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/440,725A
FILING DATE: 08-MAY-1995
                                                                                                                               2 GAGCTGCTTGGTCAGACTTATCCAGATTCTTGGCGG 37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          211 CIGCITCGTCACTCTTATCCACCTTCTTGATGAT 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       5 CTGCTTGGTCAGACTTATCCAGATTCTTGGCGGT 38
                                                 54.0%; Scor. 75.0%; Pred. No. 50, 75.0%; O; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 53.0%; Score 21.2; D
Best Local Similarity 76.5%; Pred. No. 11;
Matches 26; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; Sequence 4, Application PC/TUS9515991
                                                       Query Match
Best Local Similarity 75.09
Matches 27; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH: 282 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HYPOTHETICAL: N
HANTI-SENSE: NO
US-08-440-725A-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MOLECULE TYPE:
             ; ORGANISM: Human
US-09-949-016-14381
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COUNTRY: US
ZIP: 92037
                                                                                                                                                                                                              RESULT 7
US-08-440-725A-4/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 8
PCT-US95-15991-4/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    셤
                                                                                                                                 ઠે
```

```
ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                 APPLICANT: Crossin, Kathryn L.
APPLICANT: Sporns, Olaf
APPLICANT: Sporns, Olaf
APPLICANT: Krushel, Leslie
TITLE OF INTENTION: INHIBITION OF GLIAL CELL PROLIFERATION
NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
ADDRESSEE: Olson & Hierl, Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 6; Length 282;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-08-440-725A-7/C

Sequence 7, Application US/08440725A

Sequence 7, Application US/08440725A

Patent No. 595822

APPLICANT: Edelman, Gerald M.

APPLICANT: Scoresin, Kathryn L.

APPLICANT: Scoresin, Acathryn L.

APPLICANT: Scoresin, INTIBITION OF GLIAL CELL PROLIFERATION INTIBE OF SEQUENCES: 10

CORRESPONDENCE ADDRESS:

ADDRESSEE: THE SCRIPPS RESEARCH INSTITUTE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indela
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE: THE SCRIPPS RESEARCH INSTITUTE
STREET: 10550 No. 5985822th Torrey Pines Road, TPC-8
CITY: La Jolla
                                                                                                                                                                                                                                                                                                                                                                                                      CURRENT APPLICATION DATA:

CURRENT APPLICATION DATA:

APPLICATION NUMBER: PCT/US95/15991
FILING DATE: 11-DEC-1995
CLASSIFICATION NUMBER: PCT/US95/15991
FILING DATE: 01-DEC-1994
APPLICATION NUMBER: US 08/440,725
FILING DATE: 08-DEC-1994
APPLICATION NUMBER: US 08/440,725
FILING DATE: 08-DEC-1994
ATTONNEY/AGENT INFORMATION:
NAME: CEPURITIS, TAILVAIDIS
REGISTRATION NUMBER: 20,818
REFREENCE/DOCKET NUMBER: 15RI 457.1
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 282 base pairs
TYPE: MOLGIC acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      211 crecricercarcrirarcaccriritarian 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          5 CTGCTTGGTCAGACTTATCCAGATTCTTGGCGGT 38
                                                                                                                                                                ADDRESSEE: Olson & Hierl, Ltd.
STREET: 20 North Wacker Drive Suite 3000
CITY: Chicago
STATE: 1L
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; Score 21.2; DE; Pred. No. 11; 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
APPLICANT: Edelman, Gerald M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 53.0%;
Best Local Similarity 76.5%;
Matches 26; Conservative (
                                                                                                                                                                                                                                                                                   ZIP: 60606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gallus gallus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ORGANISM: Gallus garanti TISSUB TYPE: Brain PCT-US95-15991-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MOLECULE TYPE: CDNA HVDOTHRTICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                linear
```

```
NAME: Cepuritis, Talivaldis
REGISTRATION NUMBER: 20,818
REPERENCE/DOCKET NUMBER: TSRI
TELECOMMUNICATION INFORMATION:
TELECHANE: 312-580-1180
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 334 Dase pairs
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 334 Dase pairs
TYPE: nucleic acid
TYPE: nucleic acid
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                            TOPOLOGY: linear

MOLECTLE TYPE: CDNA

HYPOTHETICAL: NO

ANTI-SENSE: NO

PCT-US95-15991-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 11
US-09-949-016-167503/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; TYPE: DNA
; ORGANISM: Human
US-09-949-016-167503
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 2; Length 334;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 7. Application PC/TUS9515991
GENERAL INFORMATION:
APPLICANT: Edelman, Gerald M.
APPLICANT: Crossin, Kathryn L.
APPLICANT: Sporns, Olaf
APPLICANT: Krushel, Leslie
APPLICANT: Krushel, Leslie
APPLICANT: Krushel, INHIBITION OF GLIAL CELL PROLIFERATION
NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
ADDRESSEE: 0lson & Hierl, Ltd.
STREET: 20 North Wacker Drive Suite 3000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                          COMPUTE: 7237
COMPUTE: 7237
COMPUTE: Ploppy disk
COMPUTER: Ploppy disk
COMPUTER: Ploppy disk
COMPUTER: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: U$/08/440,725A
FILING DATE: 08-MAY-1995
CLASSIFICATION: 424
PRICK APPLICATION DATA:
APPLICATION NUMBER: U$ 08/353,658
FILING DATE: 09-DEC-1994
ATTORNEY/AGENT INFORMATION:
NAME: Holmes, Emily
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STATE: IL.
COUNTRY: USA
ZIP: 60606
COMPUTER: FLOPPY disk
COMPUTER: FLOPPY disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATEMET Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/15991
FILING DATE: 11-DEC-1995
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 225 crecricercarrerrarceacerrerrearear 192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        5 CTGCTTGGTCAGACTTATCCAGATTCTTGGCGGT 38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 53.0%; Score 21.2; D
Best Local Similarity 76.5%; Pred. No. 12;
Matches 26; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                   NAME: Holmes, Emily
REGISTRATION NUMBER: 40,652
REFERENCE/DOCKET NUMBER: 15R1 457.1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 784-2937
TELEPHONE: (619) 784-2939
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 334 base pairs
LENGTH: nucleic acid
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/353,658
FILING DATE: 09-DEC-1994
APPLICATION NUMBER: US 08/440,725
FILING DATE: 08-MAY-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MOLECULE TYPE: CDNA HYPOTHETICAL: NO ANTI-SPACE
California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Chicago
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 10
PCT-US95-15991-7/c
                                           92037
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-08-440-725A-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ઠ
```

```
Sequence 167503, Application US/09949016

Sequence 167503, Application US/09949016

Patent No. 6812339

GENERAL INFORMATION:

APPLICANT: VENYTER, J. Craig et al.

TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF;

FILE REPERENCE: CLOOL307

CURRENT APPLICATION NUMBER: US/09/949,016

CURRENT PILING DATE: 2000-04-14

PRIOR APPLICATION NUMBER: 60/231,768

PRIOR FILING DATE: 2000-10-20

PRIOR FILING DATE: 2000-10-03

PRIOR FILING DATE: 2000-09-08

NUMBER OF SEQ ID NOS: 207012

SOFTWARE: PRESENCE OF WINDOWS Version 4.0

SEQ ID NO 167503

LENGTH: 601
                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
Query Match 53.0%; Score 21.2; DB 6; Length 334; Best Local Similarity 76.5%; Pred. No. 12; Matches 26; Conservative 0; Mismatches 8; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
52.0%; Score 20.8; DB 3; Length 6
Best Local Similarity 70.0%; Pred. No. 21;
Matches 28; Conservative 0; Mismatches 12; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Peter Bjarke Olsen
TITLE OF INVENTION: Methods For Monitoring Multiple Gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        203 AGATCAGCTGGGACTGACTAAGCCTGAGTCTGGGCAGTGG 164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 AGAGCTGCTTGGTCAGACTTATCCAGATTCTTGGCGGTAG 40
                                                                                                                                                                                          225 crectrostroritaricacciricardar 192
                                                                                                                             5 CTGCTTGGTCAGACTTATCCAGATTCTTGGCGGT 38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-09-533-559-5575/c

Sequence 5575, Application US/09533559
Patent No. 6902897;
GENERAL INFORMATION:
APPLICANT: Randy M. Berka
APPLICANT: Michael W. Rey
APPLICANT: Jeffrey R.Shuster
APPLICANT: Jeffrey R.Shuster
APPLICANT: Laskari Kauppinen
APPLICANT: Ib Groth Clausen
```

```
Search completed: April 18, 2006, 19:31:16
Job time : 75.5 secs
                                                                                                                               TYPE: DNA
ORGANISM: Human
                                                                                                                                                                                 US-09-949-016-12760
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; ORGANISM: Human
US-09-949-016-13611
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-09-949-016-13611
                                                                                                                                                                                                                                                                                                                                                                       셤
                                                                                                                                                                                                                                                                                                                            ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 13
US-09-949-016-16464/C
US-09-949-016-16464, Application US/09949016

Sequence 16464, Application US/09949016

Sequence 16464, Application US/09949016

Sequence 16464, Application US/09949016

TITLE NO. 6812339

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

FILE REFERENCE: CL001307

CURRENT APPLICATION NUMBER: 00/241,755

PRIOR APPLICATION NUMBER: 60/241,755

PRIOR APPLICATION NUMBER: 60/241,768

PRIOR APPLICATION NUMBER: 60/231,498

PRIOR PILING DATE: 2000-10-03

PRIOR PILING DATE: 2000-09-08

NUMBER OF SEQ ID NOS: 207012

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 16464

LENGTH: 50133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 14
US-09-949-016-12760

; Sequence 12760, Application US/09949016
; Patent No. 681239
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF;
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF;
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-03
; PRIOR FILING DATE: 2000-10-03
; PRIOR PLING DATE: 2000-10-03
; PRIOR PLING DATE: 2000-10-03
                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          52.0%; Score 20.8; DB 3; Length 58133; 70.0%; Pred. No. 75; ive 0; Mismatches 12; Indels 0;
                                                                                                                                                                                                                                                                                                                                                Length 637;
                                                                                                                                                                                                                                                                                                                                           Query Match 52.0%; Score 20.8; DB 3; Length 6 Best Local Similarity 70.0%; Pred. No. 21; Matches 28; Conservative 0; Mismatches 12; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     12940 AGATCAGCTGGGACTGACTAAGCCTGAGTCTGGGCAGTGG 12901
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          308 AGGITACTIGGICACTGGIAAATAGAGICIGGGCGGIAG 269
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 AGAGCTGCTTGGTCAGACTTATCCAGATTCTTGGCGGTAG 40
                                                                                                                                                                                                                                                                                                                                                                                                                                             1 AGAGCTGCTTGGTCAGACTTATCCAGATTCTTGGCGGTAG
FILE REFERENCE: 5849.200-US
CURRENT APPLICATION NUMBER: US/09/533,559
CURRENT FILING DATE: 2000-03-22
RARLIER APPLICATION NUMBER: 09/273,623
RARLIER FILING DATE: 1999-03-22
NUMBER OF SEQ ID NOS: 7860
SEQ ID NO 5575
LENGTH: 637
                                                                                                                                                                                                                                                  ; TYPE: DNA
; ORGANISM: Aspergillus oryzae
US-09-533-559-5575
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity 70.0
Matches 28; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          g
                                                                                                                                                                                                                                                                                                                                                                                                                                             ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ઠ
```

```
Sequence 13611, Application US/09949016

Sequence 13611, Application US/09949016

Patent No. 6812339

GENERAL INPORMATION:

APPLICANT: VENTER, J. Craig et al.

ITILE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF;

FILE REPREMENTS: CLOOD-01307

CURRENT APPLICATION NUMBER: US/09/949,016

CURRENT PILING DATE: 2000-04-14

PRIOR PELING DATE: 2000-10-20

PRIOR PILING DATE: 2000-10-03

PRIOR DATE: 2000-10-03

PRIOR DATE: 2000-10-03

PRIOR DATE: 2000-10-03

PRIOR APPLICATION NUMBER: 0/231,498

NUMBER OF SEQ ID NOS: 207012

SOUTHARE: PRESENTE PRIOR WINDOWS VERSION 4.0

SEQ ID NO 13611

LENGTHERE
                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 3; Length 96074;
                                                                                                                                                                                                                                                                    DB 3; Length 96074;
                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                          71820 rrrcrcacarrrarccacarrcracaacrac 71851
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                71820 rrrengadarrranccadarrerrecaagrad 71851
                                                                                                                                                                                                                                                                                                                                                                                    9 TTGGTCAGACTTATCCAGATTCTTGGCGGTAG 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          9 TTGGTCAGACTTATCCAGATTCTTGGCGGTAG 40
                                                                                                                                                                                                                                                                 Score 20.8; DB
Pred. No. 86;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 20.8; D
Pred. No. 86;
0; Mismatches
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: PastSEQ for Windows Version 4.0
SEQ ID NO 12760
LENGTH: 96074
                                                                                                                                                                                                                                                                 Query Match 52.0%;
Best Local Similarity 78.1%;
Matches 25; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       52.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 78.1
Matches 25; Conservative
```

inis Page Blank (uspto)

```
April 18, 2006, 19:39:11; Search time 675.5 Seconds (without alignments) 489.674 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Published Applications NA Main:*

1: /cgn2_6/ptodata/1/pubpna/US07_PUBCOMB.seq:*

2: /cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq:*

3: /cgn2_6/ptodata/1/pubpna/US09A_PUBCOMB.seq:*

4: /cgn2_6/ptodata/1/pubpna/US10A_PUBCOMB.seq:*

5: /cgn2_6/ptodata/1/pubpna/US10A_PUBCOMB.seq:*

6: /cgn2_6/ptodata/1/pubpna/US10B_PUBCOMB.seq:*

7: /cgn2_6/ptodata/1/pubpna/US10B_PUBCOMB.seq:*

8: /cgn2_6/ptodata/1/pubpna/US10B_PUBCOMB.seq:*

9: /cgn2_6/ptodata/1/pubpna/US10B_PUBCOMB.seq:*

9: /cgn2_6/ptodata/1/pubpna/US10B_PUBCOMB.seq:*

10: /cgn2_6/ptodata/1/pubpna/US10B_PUBCOMB.seq:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       19587084
GenCore version 5.1.7
Copyright (c) 1993 - 2006 Biocceleration Ltd.
                                                                                                                                                                                                                                                                                                                                                            1 agagotgottggtcagacttatccagattcttggcggtag 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      9793542 seqs, 4134689005 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                     OM nucleic - nucleic search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                IDENTITY NUC Gapop 10.0 , Gapext 0.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Minimum DB seq length: 0
Maximum DB seq length: 200000000
                                                                                                                                                                                                                                                                                                 SEQ3-THEN-SEQ4
                                                                                                                                                                                                                                                                                              Title:
Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                   Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Database :
                                                                                                                                                                                                                                                                                                                                                            Sequence:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Searched:
                                                                                                                                                                               Run on:
```

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

615 38

5 CTGCTTGGTCAGACTTATCCAGATTCTTGGCGGT 582 CIGCTIGITICAGATTTATCCACATGCTTGCCAGT

ð a Sequence 523, Application US/09770445; Patent No. US20020023281A1; GENERAL INPORMATION: APPLICANT: Gorlach, Jorn; APPLICANT: An, Yong-Qiang; APPLICANT: Hamilton, Carol M.

RESULT 2 US-09-770-445-523

1, 89 1, 89 1, 89 1, 89 1, 80 1,	6
684989, 1894, Ap 200, Appl 200, Appl 34756, A 47243, A 47243, A 42393, A 42393, A 42393, A 42393, A 42393, A 42393, A 42393, A 42393, A 42391, A 42391, A 5501, Appl 1152, Appl 1152, Appl 1152, Appl 1153, A 1154, A	Gaps
Genome	, 1116; .8 0;
24 21 52.5 2291 4 US-09-255-065A-684989 58 25 21 52.5 2294 3 US-09-63-728A-36 27 20.8 52.0 247 7 US-09-63-728A-36 28 20.8 52.0 247 7 US-0-63-728A-36 29 20.8 52.0 637 8 US-09-63-728A-36 30 20.8 52.0 637 8 US-09-63-728A-35 31 20.6 51.5 367 4 US-00-525-065A-47249 32 20.6 51.5 369 7 US-10-282-122A-42393 32 20.6 51.5 369 7 US-10-282-122A-42393 33 20.6 51.5 2280 3 US-09-32-257A-18 34 20.6 51.5 2281 5 US-09-32-257A-18 35 20.6 51.5 2280 3 US-09-32-257A-18 36 20.4 51.0 0 0 US-10-282-123-13421 37 20.6 51.5 2360 7 US-10-36-31421 39 20.4 51.0 0 444 7 US-10-756-149-7272 39 20.4 51.0 640 9 US-10-26-3817-591 39 20.4 51.0 640 9 US-10-26-3817-591 30 20.4 51.0 640 9 US-10-26-3817-591 31 20.6 51.5 2280 7 US-10-21-33-1534 32 20.6 51.5 2280 7 US-10-21-33-1534 34 20.6 51.5 2280 7 US-10-21-33-1534 35 20.6 51.5 2280 7 US-10-21-33-1534 36 20.4 51.0 640 9 US-10-21-33-1534 37 20.6 51.5 20.4 51.0 640 9 US-10-21-33-1534 38 20.6 51.5 20.4 51.0 650 9 US-10-21-33-1534 39 20.4 51.0 650 9 US-10-21-33-1534 30 20.4 51.0 650 9 US-10-21-33-1534 30 20.4 51.0 600 9 US-10-21-63-817-591 30 30 30 30 30 30 30 30 30 30 30 30 30 3	Score 24.4; DB 4; Length Pred. No. 2.8; ); Mismatches 6; Indel
1291 4 US-09-925 1186 3 US-00-951 1186 3 US-00-9563 1186 3 US-09-925 1186 3 US-09-925 1186 3 US-09-925 1181 3 US-09-925 1182 3 US-09-925 1183 3 US-09-925 1184 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4	
21 52.5 2291 4 US-09-925 21 52.5 35143 5 US-0-087 21 52.5 12186 3 US-0-087 20.8 52.0 567 4 US-0-925 20.6 51.5 369 7 US-10-282 20.6 51.5 2360 3 US-0-925 20.6 51.5 2360 3 US-0-932 20.6 51.5 2360 3 US-0-936 20.6 51.5 2360 7 US-10-326 20.6 51.5 2360 7 US-10-326 20.4 51.0 544 7 US-10-326 20.4 51.0 544 7 US-10-21 20.4 51.0 543 3 US-0-925 20.4 51.0 524 4 US-0-925 20.4 51.0 526 7 US-10-021 20.4 51.0 590 7 US-10-021 20.4 51.0 S90 7 US-10-021 20.4 51.0 WUMBER: US 60/25, 147 20.4 SPERICATION NUMBER: US 60/25, 147 20.4 SPELICATION UMBER: US 60/25, 147 20.4 SPELICA	61 82 vativ
21 52.5 2291 21 52.5 3143 20.8 52.0 527 20.8 52.0 527 20.8 52.0 527 20.8 52.0 537 20.8 52.0 537 20.8 52.0 537 20.8 52.0 537 20.6 51.5 369 20.6 51.5 2360 20.6 51.5 2360 20.6 51.5 2360 20.6 51.5 2360 20.6 51.5 2360 20.6 51.5 2360 20.6 51.5 2360 20.6 51.5 2360 20.6 51.5 2360 20.6 51.5 2360 20.6 51.5 2360 20.6 51.5 2360 20.7 51.0 524 20.4 51.0 600 20.4 51.0 600 20.4 51.0 600 20.4 51.0 600 20.4 51.0 600 20.4 51.0 600 20.4 51.0 600 20.4 51.0 600 20.4 51.0 600 20.4 51.0 600 20.4 51.0 600 20.4 51.0 600 20.4 51.0 600 20.4 51.0 600 20.4 51.0 600 20.4 51.0 600 20.4 51.0 600 20.4 51.0 600 20.4 51.0 600 20.4 51.0 600 20.4 51.0 600 20.4 51.0 600 20.4 51.0 600 20.4 51.0 600 20.4 51.0 600 20.4 51.0 600 20.4 51.0 600 20.4 51.0 600 20.4 51.0 600 20.4 51.0 600 20.4 51.0 600 20.4 51.0 600 20.4 51.0 600 20.4 51.0 600 20.4 51.0 600 20.4 51.0 600 20.4 51.0 600 20.4 51.0 600 20.4 51.0 600 20.4 51.0 600 20.4 51.0 600 20.4 51.0 600 20.4 51.0 600 20.4 51.0 600 20.4 51.0 600 20.4 51.0 600 20.4 51.0 600 20.4 51.0 600 20.4 51.0 600 20.4 51.0 600 20.4 51.0 600 20.4 51.0 600 20.4 51.0 600 20.4 51.0 600 20.4 51.0 600 20.4 51.0 600 20.4 51.0 600 20.4 51.0 600 20.4 51.0 600 20.4 51.0 600 20.4 51.0 600 20.4 51.0 600 20.4 51.0 600 20.4 51.0 600 20.4 51.0 600 20.4 51.0 600 20.4 51.0 600 20.4 51.0 600 20.4 51.0 600 20.4 51.0 600 20.4 51.0 600 20.4 51.0 600 20.4 51.0 600 20.4 51.0 600 20.4 51.0 600 20.4 51.0 600 20.4 51.0 600 20.4 51.0 600 20.4 51.0 600 20.4 51.0 600 20.4 51.0 600 20.4 51.0 600 20.4 51.0 600 20.4 51.0 600 20.4 51.0 600 20.4 51.0 600 20.4 51.0 600 20.4 51.0 600 20.4 51.0 600 20.4 51.0 600 20.4 51.0 600 20.4 51.0 600 20.4 51.0 600 20.4 51.0 600 20.4 51.0 600 20.4 51.0 600 20.4 51.0 600 20.4 51.0 600 20.4 51.0 600 20.4 51.0 600 20.4 51.0 600 20.4 51.0 600 20.4 51.0 600 20.4 51.0 600 20.4 51.0 600 20.4 51.0 600 20.4 51.0 600 20.4 51.0 600 20.4 51.0 600 20.4 51.0 600 20.4 51.0 600 20.4 51.0 600 20.4 51.0 600 20.4 51.0 600 20.4 51.0 600 20.4 51.0 600 20.4 51.0 600 20.4 51.0 600 20.4 51.0 600 20.4 51.0 600 20.4 51.0 600 20.4 51.0 600 20.4 5	뎔
24 21 52.5 2291 4 US-09-925 25 21 52.5 35143 5 US-10-087 28 20.8 52.0 247 7 US-10-453 30 20.8 52.0 567 4 US-09-925 31 20.6 51.5 3280 3 US-09-925 32 20.6 51.5 3280 3 US-10-833 33 20.6 51.5 2380 3 US-10-833 34 20.6 51.5 2380 3 US-10-835 35 20.6 51.5 2380 3 US-10-835 36 20.6 51.5 2380 3 US-10-835 37 20.6 51.5 2380 3 US-10-835 38 20.4 51.0 391 7 US-10-021 40 20.4 51.0 524 7 US-10-021 41 20.4 51.0 524 7 US-10-021 42 20.4 51.0 524 7 US-10-021 43 20.4 51.0 526 7 US-10-021 44 20.4 51.0 526 7 US-10-021 44 20.4 51.0 526 7 US-10-021 45 20.4 51.0 526 7 US-10-021 47 20.4 51.0 526 7 US-10-021 48 20.4 51.0 526 7 US-10-021 49 20.4 51.0 058 US-10-021 41 20.4 51.0 058 US-10-021 42 20.4 51.0 0590 US-10-021 43 20.4 51.0 050 US-10-021 44 20.4 51.0 050 US-10-021 45 20.4 51.0 050 US-10-021 46 20.4 51.0 050 US-10-021 47 20.4 51.0 050 US-10-021 48 20.4 51.0 050 US-10-021 49 20.4 51.0 US-10-021 40 20.4 51.0 US-10-021 41 20.4 51.0 US-10-021 42 20.4 51.0 US-10-021 43 20.4 51.0 US-10-021 44 20.4 51.0 US-10-021 45 20.4 51.0 US-10-021 46 20.4 51.0 US-10-021 47 20.4 51.0 US-10-021 48 20.4 51.0 US-10-03-08 45 20.4 51.0 US-10-03-08 46 20.4 51.0 US-10-03-08 47 20.4 51.0 US-10-03-08 48 20.4 51.0 US-10-03-08 48 20.4 51.0 US-10-03-08 49 20.4 51.0 US-10-03-08 40 20.4 51.0 US-10-03-08 41 20.4 51.0 US-10-03-08 41 20.4 51.0 US-10-03-08 41 20.4 51.0 US-10-03-08 42 20.4 51.0 US-10-03-08 43 20.4 51.0 US-10-03-08 44 20.4 51.0 US-10-03-08 45 20.4 51.0 US-10-03-08 46 20.4 51.0 US-10-03-08 47 20.4 51.0 US-10-03-08 48 20.4 51.0 US-10-03-08 49 20.4 51.0 US-10-03-08 40 20.4 51.0 US-10-03-08 41 20	
24 21 52.  2 25 21 52.  2 3 20.8 52.  2 3 20.8 52.  2 3 20.8 52.  2 3 20.8 52.  2 3 20.8 52.  2 3 20.6 51.  2 3 20.6 51.  2 3 20.6 51.  2 3 20.6 51.  2 3 20.6 51.  3 3 20.4 51.  3 8 20.4 51.  4 4 20.4 51.  4 4 20.4 51.  5 43 20.4 51.  6 43 20.4 51.  7 44 20.4 51.  8 5 2 2 3 4 51.  7 44 20.4 51.  8 5 2 3 5 2 3 5 2 3 5 2 3 5 3 5 2 3 5 3 5	Query Matcl Best Local Matches

```
APPLICANT: CONTRERAS, ROLAND HENRI
APPLICANT: CONTRERAS, ROLAND HENRI
APPLICANT: BERHARDT, INES
APPLICANT: BUTTEN, WALTER HERAMAN MARIA LOUIS
APPLICANT: LUTTEN, WALTER HERAMAN MARIA LOUIS
APPLICANT: REKMANNS, REKA JOSEPHINA
TITLE OF INVENTION: YEAST AND FUNG!
FILE REFERENCE: JAB-1667
CURRENT APPLICATION NUMBER: US/10/451,467A
CURRENT APPLICATION NUMBER: EP 00870318.3
PRIOR PILING DATE: 2003-06-19
PRIOR PLING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: EP 01870002.1
PRIOR PLING DATE: 2001-01-04
PRIOR PLING DATE: 2001-01-09
PRIOR FILING DATE: 2001-01-09
NUMBER OF SEQ ID NOS: 732
SOFTWARE: Patentin version 3.1
SEQ ID NO 501
MANDER OF SEQ ID NOS: 732
MANDER OF SEQ ID NOS: 733
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 22.6; DB 7; Length 2091; Pred. No. 21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1870 GCTGCTAGACCAGTCATATCAAGATTATTGGAGGTTG 1906
276 GAGCTGCTGTGCCCAGCTCATCCAGATTCTTGCTGGT 312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        4 GCTGCTTGGTCAGACTTATCCAGATTCTTGGCGGTAG 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: ANDO, SELKO
APPLICANT: HAYASH!, MIKIRO
APPLICANT: CCHIAI, KEIKO
APPLICANT: OCHIAI, KEIKO
APPLICANT: YOKOI, HARUHIKO
APPLICANT: SENOH, AKIHIRO
APPLICANT: OZAKI, AKI
CURRENT PAPLICATION: NOVEL POLYNUCLEOTIDES
FILE REFERENCE: 249-125
CURRENT APPLICATION WHERE: JP 99/377484
PRIOR FILING DATE: 1999-12-16
PRIOR FILING DATE: 2000-04-07
PRIOR FILING DATE: 2000-04-07
PRIOR FILING DATE: 2000-08-03
NUMBER OF SEQ ID NOS: 7059
SOFTWARE: PATENT NOS: 7059
SOFTWARE: PATENT NOS: 7059
SOFTWARE: PATENT NOS: 7059
SEQ ID NO 1385
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Mismatches
                                                                                                                                    US-10-451-467A-501
Sequence 501, Application US/10451467A
; Publication No. US2040161840A1
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-09-738-626-1385/c
; Sequence 1385, Application US/09738626
; Sequence 10. US20020197605A1
; GENERAL INFORMATION:
APPLICANT: NAKAGAWA, SATOSHI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; TYPE: DNA; OSTANISM: Corynebacterium glutamicum US-09-738-626-1385
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                56.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MIZOGUCHI, HIROSHI
ANDO, SEIKO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: DNA
ORGANISM: Candida albicans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 56.5
Best Local Similarity 75.7
Matches 28; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-10-451-467A-501
셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 495, Application US/10723860
Publication No. US20040253606A1
GENERAL INFORMATION:
APPLICANT: A1. Natasha
APPLICANT: Ginsburg, Wendy M.
APPLICANT: Ginsburg, Wendy M.
APPLICANT: Zlotnik, Albert
TITLE OF INVENTION: Methods of Diagnosis of Soft Tissue Sarcoma, Compositions FITLE REPERENCE: 05882.0193.NPUS01
CURRENT APPLICATION NUMBER: US/10/723,860
CURRENT FILING DATE: 2003-11-26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 413;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 58.0%; Score 23.2; DB 3; Length 881; Best Local Similarity 77.8%; Pred. No. 9.2; Matches 28; Conservative 0; Mismatches 8; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE OF INVENTION: EXPERSED Sequences of Arabidopsis; IITLE OF INVENTION: thaliana; FILE REPERENCE: 2023US (PRARA-012PRV); CURRENT APPLICATION NUMBER: US/09/770,445; PRIOR FILING DATE: 2001-01-26; PRIOR FILING DATE: 2000-01-27; NUMBER OF SEQ ID NOS: 999; SEQ ID NO 523 ERSEQ for Windows Version 4.0; SEQ ID NO 523
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 177 AGCTGCAATGTCATACTTATCAGGTTTCTTGGAGGT 212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3 AGCTGCTTGGTCAGACTTATCCAGATTCTTGGCGGT 38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
56.5%; Score 22.6; DB 8;
Best Local Similarity 75.7%; Pred. No. 14;
Matches 28; Conservative 0; Mismatches 9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION NUMBER: 60/429,739
PRIOR FILING DATE: 2002-11.26
NUMBER OF SEQ ID NOS: 8393
SOFTWARE: Patentin version 3.2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME/KEY: misc_feature

) LOCATION: (1)...(881)

) CTHER INFORMATION: n = A,T,C or G

US-09-770-445-523
                                                                                                                                                                                                                                            Woessner, Jeffrey P
Haas, William David
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ORGANISM: Arabidopsis thaliana
                                                                                                                                                                 Matthew, Abraham V. Ledford, Brooke L.
                                                                Yu, Yang
Rameaka, Joshua G.
Price, Jennifer L.
                                       Raines, Tracy M.
                                                                                                                                                                                                                                                                                                                                                                                                                 Davis, Keith R. Allen, Keith
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Hoffman, Neil
Hurban, Patrick
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 3
US-10-723-860-495
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-10-723-860-495
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQ ID NO 495
LENGTH: 413
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: DNA
                                                                                                                                                                                                                                            APPLICANT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             셤
```

2 GAGCTGCTTGGTCAGACTTATCCAGATTCTTGGCGGT 38

ô

Gaps

```
US-10-895-849-1/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-09-938-540-1/c
                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 1294
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-10-495-066-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ò
                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               - See File Wrapper or PALM
                                                                                                                                                                                                                                                                                                                                                                                                                                        GAPLICANT: Pompelous, Markus
APPLICANT: Kroger, Burkhard
APPLICANT: Schroder, Hartwig
APPLICANT: Schroder, Hartwig
APPLICANT: Schroder, Hartwig
APPLICANT: Schroder, Gregor
APPLICANT: Aberhauer, Gregor
TITLE OF INVENTION: CORYNEBACTERIUM GLUTAMICUM GENES ENCODING
TITLE OF INVENTION: CORYNEBAC: 2004-12-06
CURRENT PILLING DATE: 2004-12-06
FRICH FILING DATE: 1999-06-23
FRICH RILLING DATE: 1999-06-25
FRICH APPLICATION NUMBER: 60/151251
FRICH APPLICATION NUMBER: 60/151251
FRICH RILLING DATE: 1999-07-01
FRICH RILLING DATE: 1999-07-07
FRICH RILLING DATE: 1999-07-07
FRICH RILLING DATE: 1999-07-07
FRICH APPLICATION NUMBER: DE 19931420.9
FRICH APPLICATION NUMBER: DE 19931221
FRICH APPLICATION NUMBER: DE 1993122.1
FRICH APPLICATION NUMBER: DE 1993-07-09
FRICH RILLING DATE: 1999-07-09
FRICH RILLING 
                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ch 55.5%; Score 22.2; DB 10; Length 1230;
1 Similarity 88.9%; Pred. No. 27;
24; Conservative 0; Mismatches 3; Indels 0;
   DB 3; Length 1107;
                                                                   Indels
55.5%; Score 22.2; I 88.9%; Pred. No. 27; ive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              704 ccercararccacarrerreceedad 678
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            14 CAGACTTATCCAGATTCTTGGCGGTAG 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: DNA ORGANISM: Corynebacterium glutamicum
                                                                                                                                                                                                                                                                                       RESULT 6
US-11-006-098-301/c
Sequence 301, Application US/11006098
Publication No. US20050153402A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 1, Application US/10495066; Publication No. US20050014234A1; GENERAL INFORMATION: APPLICANT: Zelder, Oskar APPLICANT: Pompejus, Markus; APPLICANT: Schroder, Hartwig
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LOCATION: (101)..(1207)
STHER INFORMATION: RXS00205
                                                                24; Conservative
                                                                                                                            14 CAGACTTATCCAGAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity
Query Match
Best Local Similarity
Matches 24; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 7
US-10-495-066-1/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME/KEY: CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-11-006-098-301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQ ID NO 301
LENGTH: 1230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         g
                                                                                                                                                                                         g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ò
```

```
Sequence 1, Application US/09938540

Sequence 1, Application US/09938540

Sequence 1, Application US/09938540

GENERAL INFORMATION:
APPLICANT: Degussa AG

TILLE OF THE REFERENCE: 000059 BT

CURRENT APPLICATION NUMBER: US/09/938,540

CURRENT FILLING DATE: 2011-08-27

NUMBER OF SEQ ID NOS: 4

SOFTWARE: PatentIn Ver. 2.1

SEQ ID NO 1

LENGTH: 1600

TYPE: DA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Degussa AG
TITLE OF INVENTION: New nucleotide sequences which code for the ccpAl gene
FILE REFERENCE: 000059 BT
CURRENT APPLICATION NUMBER: US/10/895,849
CURRENT FILING DATE: 2004-07-22
PRIOR APPLICATION NUMBER: US/09/938,540
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    55.5%; Score 22.2; DB 8; Length 1294; 88.9%; Pred. No. 28; tive 0; Mismatches 3; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 3; Length 1600;
APPLICANT: Klopprogge, Corinna
APPLICANT: Haberhuer, Gregor
TITLE OF INVENTION: Genes coding for regulatory proteins
FILE REPERENCE: BGI-164US
CURRENT APPLICATION NUMBER: US/10/495,066
PRIOR APPLICATION NUMBER: PCT/EP02/12139
PRIOR PILING DATE: 2002-10-31
PRIOR PLING DATE: 2002-10-31
PRIOR PLING DATE: 2001-11-05
NUMBER OF SEQ ID NOS: 76
SEQ ID NO 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 55.5%; Score 22.2; L
Best Local Similarity 88.9%; Pred. No. 29;
Matches 24; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              861 CCGTCATATCCAGATTCTTGGCGGTAG 835
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   985 ccercararccacarrerreceerae 959
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             14 CAGACTTATCCAGATTCTTGGCGGTAG 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CTTGGCGGTAG 40
                                                                                                                                                                                                                                                                                                                                            TYPE: DNA ORGANISM: Corynebacterium glutamicum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ORGANISM: Corynebacterium glutamicum FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 1, Application US/10895849
Publication No. US20050032179A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME/KEY: CDS
; LOCATION: (225)..(1388)
; OTHER INFORMATION: ccpAl-Gen
US-09-938-540-1
                                                                                                                                                                                                                                                                                                                                                                                          FEATURE:
NAME/KEY: CDS
LOCATION: (101)...(1264)
OTHER INFORMATION: RXA00205
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 88.9
Matches 24; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     14 CAGACTTATCCAGATI
```

```
CURRENT APPLICATION NUMBER: US/09/925,065A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 13
US-09-925-065A-683526
; Sequence 683526, Application US/09925065A
; Publication No. US20050228172A9
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best Local Similarity 73.7
Matches 28; Conservative
                                                                                                                                                                                                                                                                                                                                                                        TYPE: DNA
CORGANISM: Homo sapiens
US-09-925-065A-381434
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; ORGANISM: Homo sapiens
US-09-925-065A-269626
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-09-925-065A-269626
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               셤
                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 3309400;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 381434, Application US/09925065A
Publication No. US20050228172A9
GENERAL INFORMATION:
APPLICANT: Wang, David G.
TITLE OF INVERMION: Identification and Mapping of Single
TITLE OF INVERMION: Molectide Polymorphisms in the Human Genome
FILE REFERENCE: 108827.135
                                                                                                                                                                                                                                                                                                                                                     ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                       DB 8; Length 1600;
                                                                                                                                                                                                                                                                                                                                                  3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 55.5%; Score 22.2; DB 3; Best Local Similarity 88.9%; Pred. No. 1.7e+02; Matches 24; Conservative 0; Mismatches 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1317041 ¢cércararccaéarrcrigécégrae 1317015
                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 88.9%; Pred. No. 29;
Matches 24; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TITLE OF INVENTION: NOVEL POLYNUCLECTIDES
FILE REFERENCE: 249-125
CURRENT APPLICATION NUMBER: US/09/738,626
CURRENT FILING DATE: 1999-12-16
PRIOR APPLICATION NUMBER: UP 99/377484
PRIOR APPLICATION NUMBER: UP 09/159162
PRIOR APPLICATION NUMBER: UP 00/159162
PRIOR FILING DATE: 2000-04-07
PRIOR APPLICATION NUMBER: UP 00/280988
PRIOR SEQ ID NOS: 7059
SOFTWARE: PALENTIN VET. 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                           985 CCGTCATATCCAGATTCTTGGCGGTAG 959
                                                                                                                                                                                                                                                                                                                                                                                              14 CAGACTTATCCAGATTCTTGGCGGTAG 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   14 CAGACTTATCCAGATTCTTGGCGGTAG 40
                                                                                                            TYPE: DNA ORGANISM: Corynebacterium glutamicum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ORGANISM: Corynebacterium glutamicum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; Sequence 1, Application US/09738626; Publication No. US20020197605A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: NAKAGAWA, SATOSHI
APPLICANT: MIZOGUCHI, HIROSHI
APPLICANT: ANDO, SEIKO
APPLICANT: HAYASHI, MIKIRO
APPLICANT: OCHIAI, KEIKO
APPLICANT: YOKOI, HARUHIKO
APPLICANT: TATEISHI, NAOKO
APPLICANT: SENOH, AKIHIRO
APPLICANT: IKEDA, MASATO
                                                                                                                                                                          ; NAME/KEY: CDS
; LOCATION: (225)..(1388)
; OTHER INFORMATION: ccpAl-Gen
US-10-895-849-1
PRIOR FILING DATE: 2001-08-27
                   NUMBER OF SEQ ID NOS: 4
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 1
LENGTH: 1600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-09-925-065A-381434/C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            OZAKI,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQ ID NO 1
LENGTH: 3309400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 10
US-09-738-626-1/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-09-738-626-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT:
                                                                                                                                                            FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                         g
                                                                                                                                                                                                                                                                                                                                                                                                   ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            셤
```

```
ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 26926, Application US/09925065A

Publication No. US20050228172A9

FULL GENERAL INFORMATION:

APPLICANT: Wang, David G.

TITLE OF INVENTION: Identification and Mapping of Single

TITLE OF INVENTION: Noclectide Polymorphisms in the Human Genome

TITLE OF INVENTION: Noclectide Polymorphisms in the Human Genome

TITLE OF INVENTION: Noclectide Polymorphisms in the Human Genome

TITLE OF INVENTION: Noclectide Polymorphisms in the Human Genome

TITLE OF INVENTION: Noclectide Polymorphisms in the Human Genome

FILE REPERENCE: 108027.135

CURRENT FILING DATE: 2001-08-08

FRIOR APPLICATION NUMBER: US 60/252,147

FRIOR APPLICATION NUMBER: US 60/250,092

FRIOR APPLICATION NUMBER: US 60/250,092

FRIOR APPLICATION NUMBER: US 60/261,766

FRIOR APPLICATION NUMBER: US 60/261,766

FRIOR APPLICATION NUMBER: US 60/261,766

FRIOR APPLICATION NUMBER: US 60/260,092

NUMBER OF SEQ ID NOS: 957086

SEQ ID NO 269626

LENGTH: 634
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               55.0%; Score 22; DB 4; Length 634; 73.7%; Pred. No. 29; ive 0; Mismatches 10; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 55.0%; Score 22; DB 4; Length 619; Best Local Similarity 78.1%; Pred. No. 29; Matches 6; Indels Matches 6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  361 GAGCTTCTTTGTCAGTCTTACACAGAATTTTGTTGGAA 398
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2 GAGCTGCTTGGTCAGACTTATCCAGATTCTTGGCGGTA 39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               538 rregacadacraaracagraacrregereras 507
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            9 TIGGICAGACTIAICCAGATICTIGGCGGTAG 40
CURRENT FILING DATE: 2001-08-08
PRIOR APPLICATION NUMBER: US 60/243,096
PRIOR FILING DATE: 2000-10-24
PRIOR FILING DATE: 2000-11-20
PRIOR FILING DATE: 2000-11-20
PRIOR FILING DATE: 2000-11-30
PRIOR FILING DATE: 2000-11-30
PRIOR FILING DATE: 2001-01-6
PRIOR FILING DATE: 2001-01-16
PRIOR FILING DATE: 2001-01-16
PRIOR FILING DATE: 2001-01-16
PRIOR FILING DATE: 2001-05-09
NUMBER OF SEQ ID NOS: 957086
SOUTWARE: PRESERG FOR WINDOWS VERSION 4.0
SEQ ID NO 381434
```

```
Search completed: April 18, 2006, 23:14:02
Job time : 680.5 secs
                                                                                                                                                                                                                                                                                                                                                                        ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 15
US-10-767-701-19730/C
Sequence 19730, Application US/10767701
Sequence 19730, Application US/10767701
GENERAL INFORMATION:
JAPPLICANT: Kovalic, David K.
JAPPLICANT: Cao, Yinua
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Dlants and Uses Thereof For Plant Improvement
TITLE OF INVENTION: 191ants and Uses Thereof For Plant Improvement
FILE REFERENCE: 38-21(53535)B
CURRENT APPLICATION NUMBER: US/10/767,701
CURRENT FILING DATE: 2004-01-29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
TITLE OF INVENTION: Identification and Mapping of Single TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match

54.0%; Score 21.6; DB 8; Length 400660;

Best Local Similarity 75.0%; Pred. No. 2e+02;

Matches 27; Conservative 0; Mismatches 9; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 4; Length 1544;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             9; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: David W. Morris
APPLICANT: David W. Morris
APPLICANT: Marc Malandro
TITLE OF INVENTION: Novel Therapeutic Targets in Cancer
FILE REPERENCS: 529452001600
CURRENT APPLICATION NUMBER: US/10/388,838
CURRENT FILING DATE: 2003-03-14
NUMBER OF SEQ ID NOS: 114
SOFTWARE: PRESESEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1124 Grecrecriestracaartrigaagatrereres 1159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2 GAGCTGCTTGGTCAGACTTATCCAGATTCTTGGCGG 37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2 GAGCTGCTTGGTCAGACTTATCCAGATTCTTGGCGG 37
                    TITLE OF INVENTION: NUCLECTION OF THE PROPERTY OF THE REFERENCE: 10887.135
CURRENT APPLICATION NUMBER: US/09/925,065A
CURRENT PILING DATE: 2001.08-08
PRIOR PILING DATE: 2000.10-24
PRIOR PLING DATE: 2000-10-24
PRIOR PLING DATE: 2000-11-20
PRIOR PLING DATE: 2000-11-20
PRIOR PLING DATE: 2000-11-30
PRIOR PLING DATE: 2000-11-30
PRIOR PLING DATE: 2001-11-6
PRIOR PLING DATE: 2001-01-16
PRIOR PLING DATE: 2001-05-09
NUMBER OF SEQ ID NOS: 957086
SOFTWARE: PASESEE OF WINDOWS VERSION 4.0
SEQ ID NO 683526
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 54.0%; Score 21.6; D
Best Local Similarity 75.0%; Pred. No. 54;
Matches 27; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; Sequence 68, Application US/10388838
; Publication No. US2004018034A1
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: DNA ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ) ORGANISM: Homo sapiens
US-09-925-065A-683526
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQ ID NO 68
LENGTH: 400660
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 14
US-10-388-838-68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-10-388-838-68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ò
```

```
ö
                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                         ö
                                                                                                                                                                               Score 21.4; DB 7; Length 408;
Pred. No. 48;
0; Mismatches 11; Indels
                                                                                                                                                                                                                                                                                        234 ATAGCTGACTGGGCAGTCGCATCAAGATCCTTCGCGGGA 196
                                                                                                                                                                                                                                                                 1 AGAGCTGCTTGGTCAGACTTATCCAGATTCTTGGCGGTA 39
                                                                                                 ; FEATURE:
; OTHER INFORMATION: Clone ID: LIB5049-002-R1-XP1-B3
US-10-767-701-19730
                                                                                                                                                                               Query Match 53.5%;
Best Local Similarity 71.8%;
Matches 28; Conservative (
NUMBER OF SEQ ID NOS: 63128
SEQ ID NO 19730
LENGTH: 408
                                                             TYPE: DNA
ORGANISM: Sorghum bicolor
```

inis Page Blank (uspto)

## November 2005

Published_Applications Nucleic Acid and Published_Applications Amino Acid database searches now generate two sets of results each. The Published_Applications databases have been split into two parts to reduce the amount of time required for their daily updates. This results in more machine time being available for processing searches.

Newly published applications will appear in the Published_Applications_New databases; older published applications make up the Published_Applications_Main databases.

Searches run against Nucleic Acid Published_Applications produce two sets of results, with the extensions .rnpbm (Published_Applications_NA_New).

Searches run against Amino Acid Published_Applications produce two sets of results, with the extensions .rapbm (Published_Applications_AA_New).

This Page Blank (uspto)

Sequence 742008, Sequence 774063, Sequence 4131, Ap Sequence 547094, Sequence 1160503,

Sequence 1174193. Sequence 708366, Sequence 36314, A

Sequence 36315, A Sequence 137552, Sequence 137553,

Sequence 750961 Sequence 750962

Sequence 166, App Sequence 42399, A Sequence 42399, A Sequence 868797,

Sequence 426652, Sequence 490105, Sequence 1103514

Sequence 872783, Sequence 547116, Sequence 1160525

seq3-then-seq4.rnpbn

OM nucleic

Run on:

Sequence:

```
TITLE OF INVENTION: Identification and Mapping of Single
TITLE OF INVENTION: Identification and Mapping of Single
TITLE OF INVENTION: Mucleotide Polymorphisms in the Human Genome
FILE REPERENCE: 108827.135
CURRENT APPLICATION NUMBER: US/09/925,065A
CURRENT FILING DATE: 2001-08-08
FRIOR PAPLICATION NUMBER: US 60/243,096
FRIOR PILING DATE: 2000-11-20
FRIOR PILING DATE: 2000-11-20
FRIOR PILING DATE: 2000-11-30
FRIOR PILING DATE: 2000-11-30
FRIOR PILING DATE: 2001-11-6
FRIOR PILING DATE: 2001-11-6
FRIOR PILING DATE: 2001-11-6
FRIOR PILING DATE: 2001-10-16
FRIOR PILING DATE: 2001-01-16
FRIOR FILING DATE: 2001-01-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 61.0%; Score 24.4; DB 6; Length 1116; Best Local Similarity 82.4%; Pred. No. 0.71; Matches 28; Conservative 0; Mismatches 6; Indels 0
                            US-10-750-623-2619

US-09-925-0654-426652

US-10-301-480-490105

US-10-301-480-1103514

US-09-925-0654-872783

US-09-925-0654-872783

US-09-926-0654-80-547116
                                                                                                                                                                                                                                                                US-09-978-360A-166
US-09-978-360A-166
US-09-925-065A-868797
US-09-925-065A-742008
US-09-925-065A-742008
US-09-925-065A-742008
US-10-932-182A-4131
US-10-932-182A-4131
US-10-301-480-547094
US-10-301-480-560784
US-09-925-065A-708366
US-09-925-065A-36314
US-09-925-065A-36314
US-09-925-065A-36314
US-09-925-065A-36314
US-09-925-065A-36314
US-10-301-480-137553
US-10-301-480-137553
US-10-301-480-137553
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      615
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CTGCTTGGTCAGACTTATCCAGATTCTTGGCGGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CTGCTTGTTCAGATTTATCCACATGCTTGCCAGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 2
US-10-301-480-115791
; Sequence 115791, Application US/10301480
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 14554, Application US/09925065A; Publication No. US20040181048A1; GENERAL INFORMATION:
                                                                                                       6600

5500

5500

5500

5500

5500

5500

5500

5500

5500

5500

5500

5500

5500

5500

5500

5500

5500

5500

5500

5500

5500

5500

5500

5500

5500

5500

5500

5500

5500

5500

5500

5500

5500

5500

5500

5500

5500

5500

5500

5500

5500

5500

5500

5500

5500

5500

5500

5500

5500

5500

5500

5500

5500

5500

5500

5500

5500

5500

5500

5500

5500

5500

5500

5500

5500

5500

5500

5500

5500

5500

5500

5500

5500

5500

5500

5500

5500

5500

5500

5500

5500

5500

5500

5500

5500

5500

5500

5500

5500

5500

5500

5500

5500

5500

5500

5500

5500

5500

5500

5500

5500

5500

5500

5500

5500

5500

5500

5500

5500

5500

5500

5500

5500

5500

5500

5500

5500

5500

5500

5500

5500

5500

5500

5500

5500

5500

5500

5500

5500

5500

5500

5500

5500

5500

5500

5500

5500

5500

5500

5500

5500

5500

5500

5500

5500

5500

5500

5500

5500

5500

5500

5500

5500

5500

5500

5500

5500

5500

5500

5500

5500

5500

5500

5500

5500

5500

5500

5500

5500

5500

5500

5500

5500

5500

5500

5500

5500

5500

5500

5500

5500

5500

5500

5500

5500

5500

5500

5500

5500

5500

5500

5500

5500

5500

5500

5500

5500

5500

5500

5500

5500

5500

5500

5500

5500

5500

5500

5500

5500

5500

5500

5500

5500

5500

5500

5500

5500

5500

5500

5500

5500

5500

5500

5500

5500

5500

5500

5500

5500

5500

5500

5500

5500

5500

5500

5500

5500

5500

5500

5500

5500

5500

5500

5500

5500

5500

5500

5500

5500

5500

5500

5500

5500

5500

5500

5500

5500

5500

5500

5500

5500

5500

5500

5500

5500

5500

5500

5500

5500

5500

5500

5500

5500

5500

5500

5500

5500

5500

5500

5500

5500

5500

5500

5500

5500

5500

5500

5500

5500

5500

5500

5500

5500

5500

5500

5500

5500

5500

5500

5500

5500

5500

5500

5500

5500

5500

5500

5500

5500

5500

5500

5500

5500

5500

5500

5500

5500

5500

5500

5500

5500

5500

5500

5500

5500

5500

5500

5500

5500

5500

5500

5500

5500

5500

5500

5500

5500

5500

5500

5500

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ORGANISM: Homo sapiens
   0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           JS-09-925-065A-14554
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-09-925-065A-14554
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQ ID NO 14554
LENGTH: 1116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          582
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: DNA
   υU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 14554, A
Sequence 115791,
Sequence 729200,
Sequence 140, App
Sequence 72442, A
Sequence 685851,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 381434,
Sequence 450514,
Sequence 1063923,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 269656,
Sequence 683526,
Sequence 684988,
Sequence 684989,
Sequence 347566,
Sequence 119766,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 1, Appli
Sequence 472479,
                                                                                                                                                                                                                                       April 18, 2006, 19:49:40; Search time 352 Seconds (without alignments) 457.708 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Description
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Published Applications NA New:*

1: /SIDS5/ptodata/2/pubpna/USOB NEW PUB.seq:*

2: /SIDS5/ptodata/2/pubpna/USOB NEW PUB.seq:*

3: /SIDS5/ptodata/2/pubpna/USOF NEW PUB.seq:*

4: /SIDS5/ptodata/2/pubpna/PCT NEW PUB.seq:*

5: /SIDS5/ptodata/2/pubpna/NSOP NEW PUB.seq:*

7: /SIDS5/ptodata/2/pubpna/USOP NEW PUB.seq:*

8: /SIDS5/ptodata/2/pubpna/USOP NEW PUB.seq:*

9: /SIDS5/ptodata/2/pubpna/USOF NEW PUB.seq:*

10: /SIDS5/ptodata/2/pubpna/USOF NEW PUB.seq:*

11: /SIDS5/ptodata/2/pubpna/USOF NEW PUB.seq:*

12: /SIDS5/ptodata/2/pubpna/USOF NEW PUB.seq:*

13: /SIDS5/ptodata/2/pubpna/USOF NEW PUB.seq:*

14: /SIDS5/ptodata/2/pubpna/USOF NEW PUB.seq:*

15: /SIDS5/ptodata/2/pubpna/USOF NEW PUB.seq:*

16: /SIDS5/ptodata/2/pubpna/USOF NEW PUB.seq:*

17: /SIDS5/ptodata/2/pubpna/USOF NEW PUB.seq:*

18: /SIDS5/ptodata/2/pubpna/USOF NEW PUB.seq:*

18: /SIDS5/ptodata/2/pubpna/USOF NEW PUB.seq:*

18: /SIDS5/ptodata/2/pubpna/USOF NEW PUB.seq:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            18562198
                                GenCore version 5.1.7
Copyright (c) 1993 - 2006 Biocceleration Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 agagetgettggteagaettateeagattettggeggtag 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             6 US-09-925-065A-14554

10 US-10-301-480-115791

10 US-10-310-480-115791

10 US-10-310-480-729200

10 US-10-301-480-68551

10 US-10-301-480-68551

10 US-10-301-480-1053923

10 US-10-301-480-1053923

10 US-09-925-065A-683526

10 US-09-925-065A-684988

10 US-09-925-065A-684988

10 US-09-925-065A-684988

10 US-09-925-065A-684989

10 US-09-925-065A-684989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-10-301-480-1033175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-09-925-065A-472479
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  9281099 seqs, 2013915447 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                          - nucleic search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  IDENTITY NUC Gapop 10.0 , Gapext 0.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Minimum DB seq length: 0
Maximum DB seq length: 200000000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           <u>08</u>
                                                                                                                                                                                                                                                                                                                                                                          SEQ3-THEN-SEQ4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query
Match Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             611
110000
422
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             52.5
52.0
52.0
52.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               60.555.00
555.00
555.00
555.00
555.00
555.00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             20.8
20.8
20.8
20.8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          21.6
21
21
21
                                                                                                                                                                                                                                                                                                                                                                                                                     Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score
```

Databage

4

ö

Gaps

ö

υυυ

Result Š

Gaps

```
Sequence 468581. Application US/10301480

Fublication No. U32006057564A1

GENERAL INFORMATION:

FUBLICATION NO. U320060057564A1

GENERAL INFORMATION:

TITLE OF INVENTION: in the Human Genome

FILE REFERENCE: 108827.137

CURRENT FILING DATE: 2002-11-21

FRIOR APPLICATION NUMBER: US 60/311,695

FRIOR APPLICATION NUMBER: US 60/311,695

FRIOR PILING DATE: 2001-08-10

NUMBER OF SEQ ID NOS: 1226818

SOFTWARE: FASTSEQ for Windows Version 4.0

SEQ ID NO 685851

LENGTH: 589
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 7242, Application US/10301480

Sequence 7242, Application US/10301480

Publication No. US20060057564A1

GENERAL INFORMATION:

TITLE OF INVERTION: Identifiction and Mapping of Single Nucleotide Polymorphisms

TITLE OF INVERTION: In the Human Genome

FILE REFERENCE: 108827.137

CURRENT APPLICATION NUMBER: US/10/301,480

CURRENT APPLICATION NUMBER: US 10/215,598

PRIOR FILING DATE: 2002-08-09

PRIOR FILING DATE: 2002-08-09

PRIOR FILING DATE: 2001-08-10

NUMBER OF SEQ ID NOS: 1226818

SEQ ID NO 72442

LENGTH: 589
                                                                                                                                                                                                                                                                                            Query Match 60.5%; Score 24.2; DB 9; Length 145985; Best Local Similarity 78.4%; Pred. No. 3.7; Matches 29; Conservative 0; Mismatches 8; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                55.0%; Score 22; DB 9; Length 589; 73.7%; Pred. No. 7.6; Live 0; Mismatches 10; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                      88582 GTTGCTTCTTCAAAATTACCAAGACTCTTGGCAGTAG 88618
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     530 GAGCTTCTTTGTCAGTCTTACACAGAATTTTGTTGGAA 567
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2 GAGCTGCTTGGTCAGACTTATCCAGATTCTTGGCGGTA 39
                                                                                                                                                                                                                                                                                                                                                                                                       4 GCTGCTTGGTCAGACTTATCCAGATTCTTGGCGGTAG 40
SOFTWARE: FastSEQ for Windows Version 4.0 SEQ ID NO 140 LENGTH: 145985
                                                                                                                              FEATURE:

NAME/KEY: misc_feature

LOCATION: (1)...(145985)

OTHER INFORMATION: n = A,T,C or G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity 73.7
Matches 28; Conservative
                                                                                TYPE: DNA ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: DNA
ORGANISM: Homo sapien
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: DNA
ORGANISM: Homo sapien
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 6
US-10-301-480-685851
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-10-301-480-72442
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                         셤
                                                                                                                                                                                                                                                                                                                                                                                                       δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 729200, Application US/10301480

Fublication No. US20060057564A1

GHNERLI INPORMATION:

TITLE OF INVENTION: Identifiction and Mapping of Single Nucleotide Polymorphisms

TITLE OF INVENTION: In the Human Genome

TITLE OF INVENTION: In the Human Genome

JAILS REFERENCE: 108827.137

CURRENT APPLICATION NUMBER: US/10/301,480

CURRENT FILING DATE: 2002-08-09

FRIOR FILING DATE: 2002-08-09

FRIOR FILING DATE: 2001-08-10

NUMBER OF SEQ ID NOS: 1226818

SOFTWARE: FasteEQ for Windows Version 4.0
                GENERAL INFORMATION:

APPLICANT: Wang, David G.

TITLE OF INVENTION: Identifiction and Mapping of Single Nucleotide Polymorphisms
TITLE OF INVENTION: In the Human Genome
FILE REFERENCE: 108827.137
CURRENT APPLICATION NUMBER: US,10/301,480
CURRENT FILING DATE: 2002-11-21
PRIOR APPLICATION NUMBER: US 60/311,695
PRIOR APPLICATION NUMBER: US 60/311,695
PRIOR FILING DATE: 2001-08-10
NUMBER OF SED ID NOS: 1226818
SEQ ID NO 115791
LENGTH: LENGTH: 1116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gape
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 1116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 1116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 140, Application US/10330773
Publication No. US20060040262A1
GRNERAL INFORMATION:
APPLICANT: David W. Morris
APPLICANT: Marc Malandro
TITLE OF INVENTION: Novel Compositions and Methods in Cancer FILE REFERENCE: 529452001300
CURRENT APPLICATION NUMBER: US/10/330,773
CURRENT PAILING DATE: 2002-12-27
NUMBER OF SEQ ID NOS: 981
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 61.0%; Score 24.4; DB 10; Best Local Similarity 82.4%; Pred. No. 0.71; Matches 28; Conservative 0; Mismatches 6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 24.4; DB 9;
Pred. No. 0.71;
0; Mismatches 6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 582 crecrrerreadarrrarceacarecrreceaer 615
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             582 crecirericadarriarccacarecreccaer 615
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  5 CTGCTTGGTCAGACTTATCCAGATTCTTGGCGGT 38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           5 CTGCTTGGTCAGACTTATCCAGATTCTTGGCGGT 38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 61.0%;
Best Local Similarity 82.4%;
Matches 28; Conservative (
  Publication No. US20060057564A1
                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: DNA
CORGANISM: Homo sapien
US-10-301-480-115791
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: DNA
CORGANISM: Homo sapien
US-10-301-480-729200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 3
US-10-301-480-729200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-10-330-773-140
```

g ઠે

à g ö

ઠે

```
APPLICANT: Wang, David G.

TITLE OF INVENTION: Identifiction and Mapping of Single Mucleotide Polymorphisms
TITLE OF INVENTION: in the Human Genome
FILE REPERENCE: 108827.137
CURRENT APPLICATION NUMBER: US/10/301,480
CURRENT FAPLICATION NUMBER: US/202-11-21
PRIOR PILING DATE: 2002-11-21
PRIOR PILING DATE: 2002-09-09
PRIOR PILING DATE: 2001-08-10
NUMBER OF SEQ ID NOS: 1226818
SOFTWARE: PSELSEQ for Windows Version 4.0
SEQ ID NO 1063923
LENGTH: 621
                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 55.0%; Score 22; DB 10; Length 621; Best Local Similarity 78.1%; Pred. No. 7.7; Matches 25; Conservative 1; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 55.0%; Score 22; DB 6; Length 634; Best Local Similarity 73.7%; Pred. No. 7.8; Matches 28; Conservative 0; Mismatches 10; Indels
                                    Indels
                                    9
                                                                                                                                                             538 rricgachdacraaracagraacrricgcrerag 507
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                9 TIGGICAGACTIAICCAGATICTIGGCGGIAG 40
   Pred. No. 7.7;
1; Mismatches
                                                                                                                                                                                                                                                                                                                 Sequence 1063923, Application US/10301480 Publication No. US20060057564A1 GENERAL INFORMATION:
Best Local Similarity 78.1%;
Matches 25; Conservative :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; ORGANISM: Homo sapiens
US-09-925-065A-269626
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; ORGANISM: Homo sapien
US-10-301-480-1063923
                                                                                                                                                                                                                                                                                          US-10-301-480-1063923/c
                                                                                                  ઠ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 8

US-10-301-480-450514/c

i Sequence 450514, Application US/10301480

j Publication No. US20060057564A1

j GENERAL INFORMATION:

i TITLE OF INVENTION: Identifiction and Mapping of Single Nucleotide Polymorphisms

i TITLE OF INVENTION: In the Human Genome

j TITLE OF INVENTION: In the Human Genome

j CURRENT APPLICATION NUMBER: US/10/301,480

j CURRENT FILING DATE: 2002-11-21

j PRIOR PEDFICATION NUMBER: US 10/215,598

j PRIOR APPLICATION NUMBER: US 60/311,695

j PRIOR PILING DATE: 2001-08-10

j PRIOR PILING DATE: 2001-08-10

j NUMBER OF SEQ ID NOS: 1226818

j SOFFWARE: PSSECEED for Windows Version 4.0
                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GRUERAL INFORMATION:

APPLICANT: Wang, David G.

TITLE OP INVENTION: Identification and Mapping of Single
TITLE OP INVENTION: Nucleotide Polymorphisms in the Human Genome
FILE REPERENCE: 108627.135
CURRENT APPLICATION NUMBER: US/09/925,065A
CURRENT PILING DATE: 2001-08-08
PRIOR PELING DATE: 2000-10-24
PRIOR PILING DATE: 2000-10-24
PRIOR PILING DATE: 2000-11-20
PRIOR PELING DATE: 2000-11-30
PRIOR PELING DATE: 2000-11-30
PRIOR PILING DATE: 2000-11-30
PRIOR PILING DATE: 2001-01-16
PRIOR APPLICATION NUMBER: US 60/250,766
PRIOR APPLICATION NUMBER: US 60/261,766
PRIOR APPLICATION NUMBER: US 60/261,766
PRIOR APPLICATION NUMBER: US 60/261,766
PRIOR APPLICATION NUMBER: US 60/260,766
PRIOR APPLICATION NUMBER: US 60/289,846
PRIOR PILING DATE: 2001-01-16
PRIOR PILING DATE: 2001-01-16
PRIOR APPLICATION NUMBER: US 60/289,846
PRIOR SEQ ID NOS: 957086
SOFTWARE: PRAESEQ for Windows Version 4.0
FRANCELLE SEQ ID NOS: 957086
FRANCELLE SECOLORY AND ALTER SECOLORY AND AL
                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                              Query Match 55.0%; Score 22; DB 10; Length 589; Best Local Similarity 73.7%; Pred. No. 7.6; Matches 28; Conservative 0; Mismatches 10; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               55.0%; Score 22; DB 10; Length 621;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              S5.0%; Score 22; DB 6; Length 619; Best Local Similarity 78.1%; Pred. No. 7.7; Matches 25; Conservative 1; Migmatches
                                                                                                                                                                                                                                                   530 caccricrircricacrirracacacaarirricricaaa 567
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                9 TIGGICAGACTIAICCAGATICITGGCGGIAG 40
                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 381434, Application US/09925065A Publication No. US20040181048A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; ORGANISM: Homo sapien
US-10-301-480-450514
                                                                                                                                                                                                                                                                                                                                                                                   US-09-925-065A-381434/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-09-925-065A-381434
US-10-301-480-685851
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQ ID NO 450514
LENGTH: 621
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
```

ઠે 셤

ö

ö

10; Indels

```
Best Local Similarity 73.0%; Pred. No. 33;
Matches 27; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 347566, Application US/09925065A Publication No. US20040181048A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; ORGANISM: Homo sapiens
US-09-925-065A-684989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                   US-09-925-065A-684989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-09-925-065A-347566
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: DNA
                                                                                                                                                                                                                                  ద
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          셤
                                                                                                                                                   ઠ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                       TITLE OF INVENTION: Identification and Mapping of Single
TITLE OF INVENTION: Identification and Mapping of Single
TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
FILE REPERENCE: 108827.135
CURRENT APPLICATION NUMBER: US/09/925,065A
CURRENT FILING DATE: 2001-08-08
PRIOR APPLICATION NUMBER: US 60/243,096
PRIOR APPLICATION NUMBER: US 60/252,147
PRIOR APPLICATION NUMBER: US 60/252,147
PRIOR APPLICATION NUMBER: US 60/250,092
PRIOR FILING DATE: 2000-11-30
PRIOR FILING DATE: 2001-01-16
PRIOR FILING DATE: 2001-01-16
PRIOR FILING DATE: 2001-01-16
PRIOR FILING DATE: 2001-01-6
PRIOR FILING DATE: 2001-01-6
PRIOR FILING DATE: 2001-01-6
PRIOR FILING DATE: 2001-05-09
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 684988, Application US/09925065A

Sequence 684988, Application US/09925065A

Publication No. US20040181048A1

GENERAL INFORMATION:

ITILE OF INVENTION: Identification and Mapping of Single

ITILE OF INVENTION: Nucleotide Polymorphisms in the Human Genome

FILE REFERENCE: 108827.135

CURRENT FILING DATE: 2001-08-08

PRIOR APPLICATION NUMBER: US 60/252,147

PRIOR APPLICATION NUMBER: US 60/252,147

PRIOR PILING DATE: 2000-11-20

PRIOR PILING DATE: 2000-11-20

PRIOR PILING DATE: 2000-11-30

PRIOR PILING DATE: 2001-11-6

PRIOR PILING DATE: 2001-01-6

PRIOR PILING DATE: 2001-01-16

PRIOR PILING DATE: 2001-01-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 6; Length 1544;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            52.5%; Score 21; DB 6; Length 2291;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              9; Indels
                                                                         361 GAGCTTCTTTGTCAGTCTTACACAGAATTTTGTTGGAA 398
    2 GAGCTGCTTGGTCAGACTTATCCAGATTCTTGGCGGTA 39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1124 GIGCIGCITGGITAGAATTITGAAGATICTTCTCAG 1159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2 GAGCTGCTTGGTCAGACTTATCCAGATTCTTGGCGG 37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 54.0%; Score 21.6; D
Best Local Similarity 75.0%; Pred. No. 16;
Matches 27; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                           Sequence 683526, Application US/09925065A
Publication No. US20040181048A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-683526
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-09-925-065A-684988
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; ORGANISM: Homo sa
US-09-925-065A-684988
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
    ઠે
                                                                                   쉽
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     셤
```

```
ö
Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: Uncledide Polymorphisms in the Human Genome;
FITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome;
FILE REFERENCE: 108827.135
CURRENT PILING DATE: 2001-08-08
FRIOR PPLICATION NUMBER: US 60/243,096
FRIOR PPLICATION NUMBER: US 60/252,147
FRIOR PILING DATE: 2000-10-24
FRIOR PILING DATE: 2000-11-20
FRIOR APPLICATION NUMBER: US 60/250,092
FRIOR PILING DATE: 2000-11-16
FRIOR PILING DATE: 2001-01-16
FRIOR PILING DATE: 2001-01-16
FRIOR PILING DATE: 2001-01-16
FRIOR PILING DATE: 2001-05-09
FRIOR FILING DATE: 2000-05-09
FRIOR FILING DATE: 2000-0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ouery Match 52.5%; Score 21; DB 6; Length 2291; Best Local Similarity 73.0%; Pred. No. 33; Matches 27; Conservative 0; Mismatches 10; Indels
                                                                                                                                                          491 GCTrcarggrcagaarracrcacrrrcrrgrrggcag 527
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             491 GCTTCATGGTCAGAATTACTCACTTTCTTGTTGGCAG 527
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4 GCTGCTTGGTCAGACTTATCCAGATTCTTGGCGGTAG 40
```

```
RESULT 15
US-10-301-480-419766
; Sequence 419766
; Sequence 419766
; Sequence 419766
; Publication No. US20060057564A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identifiction and Mapping of Single Nucleotide Polymorphisms
; TITLE OF INVENTION: Identifiction and Mapping of Single Nucleotide Polymorphisms
; TITLE OF INVENTION: Identifiction and Mapping of Single Nucleotide Polymorphisms
; TITLE OF INVENTION: Identifiction and Mapping of Single Nucleotide Polymorphisms
; TITLE OF INVENTION: Identifiction and Mapping of Single Nucleotide Polymorphisms
; FILE REFERENCE: 10887.137
; CURRENT FILING DATE: 2002-11-21
; PRIOR PAPLICATION NUMBER: US 60/311,695
; PRIOR PILING DATE: 2001-08-10
; NUMBER OF SEQ ID NOS: 1226618
; SEQ ID NO 419766
; LENGTH: 611
                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  тв 0; Сарв
                                                                                                          Gaps
                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 52.0%; Score 20.8; DB 10; Length 611; Best Local Similarity 78.1%; Pred. No. 28; Onservative 0; Mismatches 7; Indels 0.
                                                   Query Match 52.0%; Score 20.8; DB 6; Length 567; Best Local Similarity 78.1%; Pred. No. 27; Matches 25; Conservative 0; Mismatches 7; Indels C
                                                                                                                                                                                                370 CTTGCTCAGAATCATCCAGATTTTAGGCCATA 401
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     371 CTTGCTCAGAATCATCCAGATTTTAGGCCATA 402
                                                                                                                                                                 8 CTTGGTCAGACTTATCCAGATTCTTGGCGGTA 39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                8 CTIGGICAGACTIAICCAGATICIIGGCGGIA 39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; TYPE: DNA
; ORGANISM: Homo sapien
US-10-301-480-419766
US-09-925-065A-347566
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Db r
                                                                                                                                                                 ò
                                                                                                                                                                                                                 셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Š
```

Search completed: April 18, 2006, 20:01:34 Job time : 353 secs This Page Blank (uspto)

OM nucleic - nucleic search, using sw model

Run on:

April 18, 2006, 19:11:02 ; Search time 948 Seconds (without alignments) 2398.458 Million cell updates/sec

SEQ4 - THEN - SEQ3 Title: Perfect score:

1 atccagattcttggcggtagagagctgcttggtcagactt 40 Sequence:

IDENTITY NUC Gapop 10.0 , Gapext 0.1 Scoring table:

5883141 seqs, 28421725653 residues Searched:

Total number of hits satisfying chosen parameters:

11766282

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

GenEmbl:* Database:

1: 90 ba: 4
2: 90 in: 4
4: 90 cnv; 4
5: 90 cnv; 5: 90 cnv; 6
6: 90 cn; 7
6: 90

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

		Description	AC130576 Rattus no	AC114229 Rattus no	AC114507 Rattus no	Continuation (10 o	X68427 S.oralis ge	BD147349 Primer fo	AX867287 Sequence	AJS05016 Homo sapi	BD158115 Primer fo	AX879955 Sequence	AK022924 Homo sapi	BD156054 Primer fo	AX876294 Sequence	AK001233 Homo sapi	BD249583 DNA repli	BC096758 Homo sapi	BC018694 Homo sapi	BD159594 Primer fo
SUMMARIES		ar	AC130576	AC114229	AC114507	CR382128 09	SO23SRRN _	BD147349	AX867287	HSA505016	BD158115	AX879955	AK022924	BD156054	AX876294	AK001233	BD249583	BC096758	BC018694	BD159594
		08	14	14	14	15	-	9	ø	00	9	9	œ	9	9	80	9	0	œ	9
		Watch Length DB	219245	222077	234153	110000	2902	871	871	2126	2343	2343	2343	2390	2390	2390	2650	2763	2823	2892
		Match	61.5	61.5	61.5	61.0	0.09	59.5	59.5	59.5	59.5	59.5	59.5	59.5	59.5	59.5	59.5	59.5	59.5	59.5
		Score	24.6	24.6	24.6	24.4	24	23.8	23.8	23.8	23.8	23.8	23.8	23.8	23.8	23.8	23.8	23.8	23.8	23.8
	16	No.	0	7	c o	4	S	9 0	0	ω U	σ 0	0 10	c 11	c 12	c 13	c 14	c 15	c 16	c 17	c 18

AX882205 Sequence	AK022573 Homo sapi	AK025149 Homo sapi	AK123857 Homo sapi	BD158653 Primer fo	AX880894 Sequence	AK023826 Homo sapi	AB007931 Homo sapi	AX677323 Sequence	AR338613 Sequence	AX780115 Sequence	CQ729868 Sequence	CQ873939 Sequence	AF348492 Homo sapi	BX890577 Zebrafish	AB103331 Mus muscu	AC127867 Rattus no	AC154141 Mus muscu	AC154658 Mus muscu	AC154737 Mus muscu	AC108967 Rattus no	D89263 Schizosacch	AL132984 S.pombe c	AC142182 Rattus no	AC135443 Rattus no	AC094057 Rattus no	AK071737 Oryza sat	
AX882205	AK022573	AK025149	AK123857	BD158653	AX880894	AK023826	AB007931	AX677323	AR338613	AX780115	CQ729868	CQ873939	AF348492	BX890577	AB103331	4 AC127867	AC154141	AC154658	I AC154737	1 AC108967	5 D89263	5 SPAC1556	1 AC142182	1 AC135443	I AC094057	5 AK071737	
9	æ	ω	æ	ø	9	æ	æ	9	9	9	ø	9	æ	S	0	14	σ	0	14	14	15	15	14	14	14	15	
2892	2892	3409	3475	6701	6701	6701	7150	7228	7827	8825	10852	15552	15552	114934	5190	171231	178391	205427	218468	245080	1585	13936	189425	223728	231785	1103	
ď.	ŝ	ī.	'n	ŝ	ŝ		ŝ	'n	'n	'n	'n	'n	ŝ	0.	'n	'n	'n	'n	'n	'n	٥.	٥.	٥.	0	٥.	'n	
5	59.	5	5	5	5	53	59	59	5	59	59	23	59	59	57	57.	57	57	57	57	57	57	57	57	57	26	
23.8	۳. ا	ë.	ë.	23.8	θ,	23.8	23.8	23.8	23.8	٠	23.8	23.8	23.8	23.6	23	23	23	23	23	23	22.8	22.8		22.8	22.8	22.6	
19	20	7	22	23	24	25	56	23	28	29	30	31	32	33	34	32	36	37	38	39	40	41	42	43	44	45	
υ	υ	υ	υ	υ	υ	υ	υ	υ	υ	υ	ט	υ	υ			υ		υ		ט	Ü	•	•	Ü	Ü	•	

## ALIGNMENTS

ACL30576 219245 bp DNA linear HTG 15-NOV-2002 Rattus norvegicus clone CH230-283D7, WORKING DRAFT SEQUENCE. ACL30576 AC130576.4 GI:25007506 HTG, HTGS PHASE2; HTGS DRAFT; HTGS_FULLTOP. Rattus norvegicus (Norway rat) Rattus norvegicus RESULT 1
AC130576/C
LOCUS
DEFINITION
ACCESSION
VERSION
VERSION
CETWORDS
SOURCE
ORGANISM

Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia, Eutheria, Euarchontoglires, Glires, Rodentia, Sclurognathi, Muroidea, Muridae, Murinae, Rattus.

REFERENCE AUTHORS

Sciurognathi, Murcidea; Muridae; Marinae; Rattus.

Sciurognathi, Murcidea; Murcidea; Marinae; Rattus.

I (bases 1 to 219245)

Muzny, D. Marie., Metzker, M. Lee., Abramzon, S., Adams, C., Alder, J.,

Allen, C., Allen, H., Alabrooks, S., Amin, A., Angulano, D.,

Allen, C., Allen, H., Alabrooks, S., Amin, A., Angulano, D.,

Allen, C., Allen, H., Ayodeji, M., Baca, B., Baden, H.,

Baldwin, D., Bandaranaike, D., Barber, M., Barnstead, M., Benahmed, F.,

Biswalo, K., Blair, J. Blankenburg, K., Blyth, P., Brown, M.,

Bryant, N., Bulay, C., Burch, P., Burrell, K., Calderon, E.,

Cardenas, V., Carter, K., Cavasos, I., Ceasar, H., Center, A.,

Clacko, J., Chavez, D., Chen, G., Chen, R., Chen, Z., Chu, J.,

Clacko, J., Chavez, D., Chen, G., Coyle, M., Cree, A., De Corkrell, R., Cox, C., Coyle, M., Cree, A., De Corkrell, C., Davis, C., Coyle, M., Cree, A., De Corkrell, Davis, C., Davis, C., Coyle, M., Cree, A., De Corgan, C., Davis, C., Coyle, M., Carter, P., Fangen, Roche, S., Dunn, A., Duva, Davis, C., Paras, C., Egan, R., Garta, R., Garter, M., Gabisi, A., Ganta, R., Gardy, M., Guerra, W., Harles, S., Hladun, S.L., Haddson, C., Hamilton, C., Hamilton, C., Hamilton, K., Harvey, Y., Havlak, P., Hawes, A., Henderson, W., Housis, L., Karpathy, S., Kally, S., Kally, S., Khan, Z., Logoon, J., Lewis, L., Lobow, H., Levan, J., Lewis, L., Loulesged, H., Lozado, R.J., Luwis, L., Loulesged, H., Lozado, R.J., Luwis, L., Loulesged, H., Lozado, R.J., Luwis, L., Loulesged, H., Levan, M., Luwis, M., Martin, K., Martin, K., Martin, K., Mangun, B., Mangun, P., Martin, K., Martin, K., Martin, K., Martin, K., Martin, K., Mangun, B., Mangun, P., Martin, K., Martin, K.,

```
Milosavljevic, A., Miner, G., Minja, E., Montemayor, J., Moore, S., Morgan, M., Morris, K., Morris, S., Munidasa, M., Murphy, M., Narris, S., Nankervis, C., Naal, D., Newton, N., Nayven, N., Norris, S., Nankervis, C., Naal, D., Newton, N., Nayven, N., Palis, S., Navelemeh, O., Okwonu, G., Olarnpunsagoon, A., Palis, Parks, K., Polidekrer, A., Polidekrer, A., Polidekrer, M., Renter, M., Richards, S., Riggs, P., Railly, B., Railly, M., Ran, Y., Reves, K., Regier, M.A., Reigh, R., Rives, C., Rodkey, T., Rojas, A., Rose, M., Rose, R., Rhiz, S. J., Shetty, J., Shartsbeyn, A., Sisson, I., Sitter, C.D., Smajs, D., Shetty, J., Shartsbeyn, A., Sisson, I., Sitter, C.D., Smajs, D., Shetty, J., Shartsbeyn, A., Sisson, I., Sitter, C.D., Smajs, D., Steinle, M., Sarong, K., Sutton, A., Svatelle, R., Sosa, J., Steinle, M., Strong, R., Sutton, A., Svatelle, R., Sosa, J., Tabor, D., Taylor, T., Thomas, N., Thomas, S., Tingey, A., Treios, Z., Usmani, K., Valas, R., Wail, K., Walter, R., Walte, F., Walliams, G., Waillams, G., Walter, R., Wooden, H., Worley, K., Wijht, D., Wright, D., Wright, R., Walss, R., Zhao, S., Dunn, D., Von, N., Weinstock, G. and Gibbs, R.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (12-AUG-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
3 (bases 1 to 219245)
Rat Genome Sequencing Consortium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2 (bases 1 to 219245)
Worley, K.C.
Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 JOURNAL
REFERENCE
AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TITLE
JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REFERENCE
AUTHORS
TITLE
JOURNAL
```

Direct Submission Called Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA On Nov 15, 2002 this sequence version replaced gi:23912386. The sequence in this assembly is a combination of BAC based reads and whole genome shocgun sequencing reads assembled using Atlas (http://www.hgsc.bcm.kcm.edu/projects/rat/). Each contig described in the feature table below represents a scaffold in the Atlas assembly (a 'contig-scaffold'). Within each contig-scaffold, individual sequence contigs are ordered and oriented, and separated by sized gaps filled with Ns to the estimated size. The sequence may extend beyond the ends of the clone and there may be sequence contigs within a contig-scaffold that consist entirely of whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence reads. Both end sequences and whole genome table. ----- Genome Center

COMMENT

```
Center Clone name: CH230-283D7
------- Summary Statistics
Assembly program: Phrap; version 0.990329
Consensus quality: 202069 bases at least Q40
Consensus quality: 204430 bases at least Q30
Consensus quality: 205755 bases at least Q20
Estimated insert size: 207591; aum-of-contigs estimation
Q20 bases; sum-of-contigs estimation
                                                   Center: Baylor College of Medicine Center code: BCM
```

```
NOTE: Bstimated insert size may differ from sequence length (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).
NOTE: This is a working draft's sequence. It currently consists of 1 contigs. Gaps between the contigs are represented as runs of N. The order of the pieces is believed to be correct as given, however the sizes of the gaps between them are based on estimates that have provided by the submittor.
This sequence will be replaced
```

```
Rattus norvegicus (Norway rat)

Enkaryota morvegicus (Norway rat)

Enkaryota metazoa Chordata Craniata; Vertebrata; Euteleostomi;

Enkaryota Merazoa Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalla; Eutheria; Euarchontogilres; Gilres; Rodentia;

Sciurognathi; Muroidea; Muridae; Murinae; Rattus.

1 (bases 1 to 22207).

Ry Muzny, D. Marie., Mete., Abramzon, S., Adams, C., Alder, J.,

Anyalebechi, V., Aoyagi, A., Ayodeji, M., Baca, E., Baden, H.,

Baldwin, D., Bandaranaike, D., Barber, M., Barastead, M., Benahmed, F.,

Biswalo, K., Blair, J., Blankenburg, K., Blyth, P., Brown, M.,

Bryant, M., Buhay, C., Blankenburg, K., Blyth, P., Brown, M.,

Eryant, M., Buhay, C., Burch, P., Burrell, K., Canderon, E.,

Cardenas, V., Carter, K., Cavazos, I., Ceasar, H., Center, A.,

Checko, J., Chavez, D., Chen, R., Chen, R., Chen, Y., Chen, Z., Chu, J.,

Claveland, C., Cockrell, R., Cox, C., Coyle, M., Cree, A., D'Souza, L.,

Davila, M.L., Davis, C., Davy-Carroll, L., De Anda, C., Dederich, D.,

Davila, M.L., Davis, C., Davy-Carroll, L., De Anda, C., Dederich, D.,

Davila, M. Escotto, M., Eugene, C., Evans, C.A., Falls, T., Fan, G.,

Fernandez, S., Falley, M., Flaggi, M., Forbes, L., Foster, M.,

Gebregeorgis, E., Geer, K., Gill, R., Garcia, A., Hongues, M.,

Hernandez, R., Hansa, R., Handen, S. L., Hunder, M., Holline, S., Hund, Y., Shan, Y., Hander, J., Jackson, A.,

Harvey, Y., Havlak, P., Hawes, A., Henderson, N., Hernandez, J., Jackson, A.,

Hallins, B., Howells, S., Hullyk, S., Hume, J., Idhebird, D., Jackson, A.,

Karpathy, S., Kelly, S., Rully, S., Khule, J., Johnson, B., Johnson, R., Johnson, C., Liu, J.,

Karpathy, S., Kelly, S., Kelly, S., Khan, Z., King, L., Kovar, C.,

Kowis, C., Kraft, C.L., Lebow, H., Levan, J., Lewis, L., Li, Z., Liu, J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AC114229
Rattus norvegicus clone CH230-322D21, *** SEQUENCING IN PROGRESS
***, 3 unordered pieces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Gaps
* by the finished sequence as soon as it is available and

* the accession number will be preserved.

* 1 122245: contig of 219245 bp in length.

Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61.5%; Score 24.6; DB 14; Length 219245; 76.9%; Pred. No. 53; ive 0; Mismatches 9; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      172592 AICCIGATTGTCGGTAGACAACAGCTTGCCCACACT 172554
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AC114229
AC114229.3 GI:23195356
HTG: HTGS PHASEL; HTGS_DRAFT; HTGS_ENRICHED.
Rattus norvegicus (Norway rat)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 ATCCAGATTCTTGGCGGTAGAGAGCTGCTTGGTCAGACT
                                                                                                                                                        /organism="Rattus norvegicus"
/mol_type="genomic DNA"
/db_xref="taxon:10116"
/clone="CH230-283D7"
                                                                                                                                                                                                                                                                                 1. .1173
/note="wgs end_extension
clone_end:Sp6"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          end_sequence:BZ257705"
217179. .219245
/note="wgs_end_extension
clone_end:T7"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       end sequence:BZ257707"
211604. .212304
/note="clone_boundary
clone_end:T7
                                                                                                                                                                                                                                                                                                                                                                               1923. . . 2795
/note="clone_boundary
clone_end:Sp6
                                                                                                                              1. .219245
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 76.94
Matches 30; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 alte.
                                                                                                                                                                                                                                                                                       misc_feature
                                                                                                                                                                                                                                                                                                                                                                                      misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
                                                                                                                                  source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 2
AC114229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REFERENCE
                                                                                           FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ò
```

arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved. is not known and their order in this sequence record is

source

FEATURES

10381: contig of 10381 bp in length
10382 10481: gap of unknown length
10482 220209: contig of 209728 bp in length
10210 220209: gap of unknown length
10210 222077: contig of 1768 bp in length
10220 177: contig of 1768 bp in length
1022077: contig of 1768 bp in length
10381 contig of

misc feature

misc_feature misc_feature

```
Submitted (10-0CT-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA

Baylor Plaza, Houston, TX 77030, USA

On Sep 19, 2002 this sequence version replaced gi:21744222.

The sequence in this assembly is a combination of BAC based reads and whole genome shotgun sequencing reads assembled using Atlas (http://www.hgsc.bcm.tmc.edu/projects/rat/). Each contig described in the feature table below represents a scaffold in the Atlas assembly (a 'contig-scaffold'). Within each contig-scaffold, individual sequence contigs are ordered and oriented, and separated by sized gaps filled with Ns to the estimated size. The sequence may extend beyond the ends of the clone and there may be sequence contigs within a contig-scaffold that consist entirely of whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence reads. Both end sequences and the feature table.
Liu, J., Liu, W., Liu, Y., London, P., Longacre, S., Lopez, J.,
Lorensuhewa, L., Loulseged, H., Lozado, R.J., Lu, X., Ma, J.,
Maheshwari, W., Malindartne, M., Mahmoud, M., Martinez, E.,
Mangum, B., Mapua, P., Martin, K., Martinez, E.,
Milosavijevic, A., Minjar, E., Montemayor, J., Moore, S.,
Minsavijevic, A., Minjar, M., Martin, Murphy, M., Noris, S.,
Morgan, M., Mortis, K., Mortis, S., Montemayor, J., Moore, S.,
Navoklemeh, O., Okwond, G., Olarnpunason, A., Pal, S., Parks, K.,
Pasternak, S., Paul, H., Perez, A., Perez, L., Pfannkoch, C.,
Plopper, F., Poindexter, A., Popovic, D., Primus, B., Pu, L.-L.,
Plopper, F., Poindexter, A., Popovic, D., Primus, S., Riggs, F.,
Raily, B., Reilly, M., Rachlin, B., Reeves, K., Rogier, M.A., Reigh, R.,
Raily, B., Reilly, M., Rachlin, E., Reeves, K., Rogier, M., Reigh, R.,
Sanders, W., Savery, G., Schorer, S., Soct, G., Shatsman, S., Shen, H.,
Shetty, J., Shvartsbeyn, A., Sisson, I., Sitter, C.D., Smajs, D.,
Steinle, M., Strong, K., Sutton, A., Svarek, A., Tabor, P., Taylor, C.,
Taylor, T., Thomas, N., Thomas, S., Tingey, A., Trejos, Z., Usmani, K.,
Valas, R., Vera, V., Villasana, D., Waldron, L., Walker, B., Wang, J.,
Wright, D., Wright, R., Walker, Weik, K., White, F.,
Wright, D., Wright, R., Walker, M., Woolen, H., Worley, K.,
Wright, D., Wright, R., Walker, S., Dunn, D., Von
Niederhausern, A., Weiss, R., Smith, H.O.,
Weinstock, G. and Gibbs, R.A., Smith, D.R., Smith, H.O.,
Willens, G., Smith, S., Smith, R., Shan, S., Smith, H.O.,
Willens, G., Smith, S., Smith, R., Smith, H.O.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2 (bases 1 to 222077)
Worley,K.C.
Submission
Submitted (07-MAR-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Quality coverage: 5x in Q20 bases; sum-of-contigs estimation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Center: Baylor College of Medicine
Center code: BCM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3 (bases 1 to 222077)
Rat Genome Sequencing Consortium.
Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -- Genome Center
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REFERENCE
AUTHORS
TITLE
JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REFERENCE
AUTHORS
TITLE
JOURNAL
```

COMMENT

ö

Gaps

ö

Indels

Score 24.6; DB 14; Pred. No. 53; 0; Mismatches 9;

61.5%;

Query Match Best Local Similarity 76.9 Matches 30; Conservative

'estimated_length=unknown 220210. .220309 /estimated_length=unknown

gap gap

ORIGIN

end_sequence:RXANO23TJ" 10382. .10001

site:MboI

1 ATCCAGATTCTTGGCGGTAGAGAGCTGCTTGGTCAGACT

셤

Length 222077;

```
SM Rattus increases (nordates) tenders (lites) Ruteleostomi, Bukaryota; Metazoa; Chordates; Claires; Rodentia; Butheria; Butheria; Buarchontoglires; Glires; Rodentia; Sciurognathi; Muroidae; Murinae; Rattus.

Sciurognathi; Muroidae; Muridae; Murinae; Rattus.

I (bases 1 to 234153)

SM Mary, D. Marie., Metzker, M.Lee., Abramzon, S., Adams, C., Alder, J., Alabrooks, S., Amin, A., Anquiano, D., Allen, H., Alabrooks, S., Amin, A., Anquiano, D., Allen, H., Bardara, M., Baca, B., Baden, H., Baldwin, D., Bandaranaike, D., Blanber, M., Barnstead, M., Benahmed, F., Baldwin, D., Bandaranaike, D., Blanber, M., Barnstead, M., Benahmed, F., Baldwin, D., Bandaranaike, D., Burch, P., Brown, M., Bryant, N., Buhay, C., Burch, P., Burrell, K., Cater, Y., Cater, Z., Cha, J., Chacko, J., Chavez, D., Chen, G., Chen, Y., Chen, Z., Chacko, J., Chavez, D., Chen, G., Chen, Y., Chen, Z., Cockrell, R., Cox, C., Coyle, M., Cree, A., Deforich, Davis, C., Devaeno, C., Devaeno, C., Davy-Carroll, L., De Anda, C., Dederich, D., Delgado, O., Denson, S., Deramo, C., Din, H., Divya, K., Bgan, M., Escetto, M., Rugene, C., Evans, C. A., Falls, T., Fernandez, S., Finley, M., Flaggy, M., Fostes, M., Garner, T., Garza, M., Fraser, C. M., Gabisi, A., Garta, R., Garcia, A., Garner, T., Garza, M.,
                                                                                                                                                                                      ACLI4507
234153 bp DNA linear HTG 15-NOV-2002
Rattus norvegicus clone CH230-30113, WORKING DRAFT SEQUENCE, 3
25944 AICCIGAITCITICCGAIAGACAACAGCITGCCCACACI 25982
                                                                                                                                                                                                                                                                                                                                                AC114507 GI:25007270
AC114507.4 GI:25007270
HTG; HTGS PHASE1; HTGS DRAFT; HTGS_FULLFOP.
Rattus noFvegicus (Norway rat)
                                                                                                                                                                                                                                                                                                                                                                                    VERSION
KEYWORDS
SOURCE
ORGANISM
                                                                                                                                                                                          AC114507/c
                                                                                                                                                                                                                                                                   DEFINITION
                                                                                                                                                                                                                                                                                                                                                ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AUTHORS
                                                                                                                                                 RESULT 3
                                                                                                                                                                                                                                  LOCUS
```

* NOTE: Estimated insert size may differ from sequence length ... (see http://www.hgsc.bcm.tuc.cdu/docs/Genbank draft data.html).

* NOTE: This is a 'working draft' sequence. It currently

* consists of 3 contigs. The true order of the pieces

Consensus quality: 220753 bases at least Q20

```
Gebregeorgis, B., Geer, K., Gill, R., Grady, M., Guerra, W., Gunaratne, P., Haaland, W., Hamil, C., Hamilton, C., Hamilton, K., Havdak, P., Hawes, A., Henderson, N., Hernandez, J., Hollins, B., Howells, S., Hulyk, S., Hume, J., Idlebird, D., Jackson, A., Jacob, L., Jiang, H., Johnson, B., Johnson, R., Loez, J., Liu, J., Liu, M., Liu, Y., London, P., Longare, S., Lopez, J., Lorensuhewa, L., Louliseged, H., Lozado, R.J., Lu, X., Ma, J., Mahebhwari, M., Mahindartne, M., Mahmoud, M., Marloy, K., Mangum, A., Mahebhwari, M., Mahindartne, M., Martinez, B., Moreens, B., Moreens, B., Moreens, R., Morgan, M., Morris, K., Morris, S., Mortemayor, J., Moore, S., Morgan, M., Morris, K., Morris, S., Munidasa, M., Murphy, M., Nair, L., Nasternak, S., Paul, H., Perez, L., Pfannkoch, C., Pasternak, S., Paul, H., Perez, L., Pfannkoch, C., Plopper, F., Poindexter, A., Popovic, D., Primus, B., Reily, M., Rahlin, B., Reves, K., Regler, M., Radhin, B., Reilly, M., Rah, Y., Rauter, M., Rabers, B., Shateman, S., Shen, H., Shetty, J., Shvartsbeyn, A., Sasery, G., Scherer, S., Scott, G., Shateman, S., Shetty, J., Shvartsbeyn, A., Sasery, G., Scherer, S., Scott, G., Shateman, S., Shen, H., Shetty, J., Shvartsbeyn, A., Sasel, R., Satton, A., Sodergren, E., Song, X.-Z., Sorelle, R., Soker, Y., Waigh, S., Waise, N., Waight, N., Waight, R., Waigh, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Direct Submission

Submitted (10-MAR-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA

3 (bases 1 to 234153)

5 Rat Genome Sequencing Consortium.

Direct Submission

Loudocular and Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA

On Nov 15, 2002 this sequence version replaced gi:22857240.

The Sequence in this assembly is a combination of BAC based reads and whole genome shotgun sequencing reads assembled using Atlas (http://www.hgsc.bcm.tmc.edu/projects/rat/). Each contig described in the fature table below represents a scaffold in the Atlas assembly (a 'contig-scaffold'). Within each contig-scaffold', Mithin each contig-scaffold, individual sequence contigs are ordered and oriented, and separated by sized gaps filled with Ns to the estimated size. The sequence may extend beyond the ends of the clone and there may be sequence contigs within a contig-scaffold that consist entirely of whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence reads.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Center: Baylor College of Medicine Center code: BCM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2 (bases 1 to 234153)
Worley, K.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Direct Submission
Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE
JOURNAL
REFERENCE
AUTHORS
TITLE
JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REFERENCE
AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE
JOURNAL
```

COMMENT

```
ö
                                                                data.html).
              Quality coverage: 7x in Q20 bases; sum-of-contigs estimation
                                       NOTE: Estimated insert size may differ from sequence length (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.h NOTE: This is a 'working draft' sequence. It currently consists of 3 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
Estimated insert size: 222569; sum-of-contigs estimation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LOCUS CR382128 Accession CR382128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 14; Length 234153;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                   228679 228778: gap of unknown length 228679 228778: gap of unknown length 228779 231809: contrig of 3031 bp in length 231810 231810 231810 231810 231810 231810 231810 231810 231810 231810 231810 231810 231810 231810 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               50632 ATCCTGATTCTTGCCGATAGACAACAGCTTGCCCACACT 50594
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 ATCCAGATTCTTGGCGGTAGAGAGCTGCTTGGTCAGACT
                                                                                                                                                                                                                                                                                                                                            /organism="Rattus norvegicus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     / Match 61.5%; Score 24.6; L
Local Similarity 76.9%; Pred. No. 53;
Nes 30; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     'estimated_length=unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /estimated_length=unknown
                                                                                                                                                                                                                                                                                                                                                           /mol_type="genomic DNA"
/db_xref="taxon:10116"
/clone="CH230-30113"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2010000
2110000
2210000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  410000
510000
610000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    710000
810000
910000
                                                                                                                                                                                                                                                                                                                                                                                                             1. .1445
/note="wgs_contig"
1496. .3185
/note="wgs_contig"
227041. .228678
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                110000
210000
310000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1110000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1410000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        010000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1310000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1610000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1710000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1810000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note="wgs_contig"
228679. .228778
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       231810. \ \ .2\overline{3}1909
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence split into 31 fragments
                                                                                                                                                                                                                                                                                                                          1, .234153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1000001
1100001
1200001
1300001
1400001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1800001
1900001
2000001
2100001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     200001
300001
400001
500001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      600001
700001
800001
900001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 100001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1600001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                700007
                                                                                                                                                                                                                                                                                                                                                                                                                misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                 misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CR382128-01

CR382128-03

CR382128-03

CR382128-05

CR382128-06

CR382128-09

CR382128-09

CR382128-11

CR382128-11

CR382128-11

CR382128-11

CR382128-11

CR382128-11

CR382128-13

CR382128-13

CR382128-14

CR382128-14

CR382128-14

CR382128-14

CR382128-14

CR382128-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CR382128_18
CR382128_19
CR382128_20
CR382128_20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Fragment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 4
CR382128 09
WPCOMMENT
                                                                                                                                                                                                                                                                                                                                source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      gap
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        gap
                                                                                                                                                                                                                                                                                                              FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ઠ
```

a

ઠે

```
Hominidae, Homo.

18 1 (bases 1 to 871)

19 Ota,T., 180gai,T., Nishikawa,T., Hayashi,K., Saito,K., Yamamoto,J.,

19 Ota,T., 180gai,T., Nishikawa,T., Hayashi,K., Saito,K., Yamamoto,J.,

19 Inhii,S., Sugiyama,T., Wakamatsu,A., Nagai,K. and Otsuki,T.

19 Primer for synthesizing full-length cDNa and use thereof

10 Primer for synthesizing full-length cDNa and use thereof

11 HELIX RESEARCH INSTITUTE

12 HELIX RESEARCH INSTITUTE

13 HOMO sapiens (human)

14 D 09-JUL-2002

15 P 2002191363-A/2192

16 D 09-JUL-2000

17 P 28-UL-2000 JP 2000280990

18 P 28-UL-2000 JP 2000280990

19 P TOSHIO OTA,TAKAO ISOGAI,TETSUO NISHIKAWA,KOJI HAYASHI,KAORU

10 JUNICHI YAMAMOTO,SHIZUKO ISHII,TOMOYASU SUGIYAMA,AI WAKAWATSU,

11 FKEIICHI NAGAI,TETSUJI OTSUKI

14 CI2NIS/09,COTKI4/47,COTKI6/18,CI2NI/15,CI2NI/21,CI2NS/ PC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PAT 17-DEC-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ota,T., Isogai,T., Nishikawa,T., Hayashi,K., Saito,K., Yamamoto,J., Ishii,S., Sugiyama,T., Wakamatsu,A., Nagai,K. and Otsuki,T. Primers for syntheselsing full-length cDNA and their use Patent: EP 1074677-A 2122 07-FBB-2001; Patent: EP 1074677-A 2122 07-FBB-2001; Research Association for Biotechnology (JP)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C C12P21/02,C12Q1/68//C12P21/08,G06F17/30,C12N15/00,C12N5/00 CC Primer for synthesizing full-length cDNA and use thereof FH Key Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Buarchontoglires, Primates, Catarrhini,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gapa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        organism='Homo sapiens (human)'.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 59.5%; Score 23.8; DB 6; Length 871; Best Local Similarity 80.0%; Pred. No. 1.3e+02; Matches 28; Conservative 0; Mismatches 7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 871;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indela
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 23.8; DB 6;
Pred. No. 1.3e+02;
0; Mismatches 7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             649 AICCAAAITCIIGGGGCTAGGAAIGTGCIITTICA 615
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        649 Arccaaarrcrrgggggrgggargrgcrrrrca 615
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 ATCCAGATTCTTGGCGGTAGAGAGCTGCTTGGTCA 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 ATCCAGATICTIGGCGGTAGAGAGCTGCTTGGTCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   871 bp Di
Sequence 2192 from Patent EP1074617.
AX867287
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1. .871
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AX867287.1 GI:40021669
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               59.5%;
80.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens (human)
Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ouery Match
Best Local Similarity 80.09
Matches 28, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               H
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AX867287/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ACCESSION
VERSION
KEYWORDS
SOURCE
                                   REFERENCE
AUTHORS
                                                                                                          TITLE
JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TITLE
JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FEATURES
                                                                                                                                                                                         COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LOCUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ठे
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ઠ
                                                                                                                                                                                                            CR382128_30 3000001 3066374
Continuation (10 of 31) of CR382128 from base 900001 (CR382128 Yarrowia lipolytica chrom
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        E liceroccues.

Indwig, W., Kirchof, G., Klugbauer, N., Weizenegger, M., Betzl, D., Eludwig, W., Kirchof, G., Klugbauer, N., Weizenegger, M., Betzl, D., Elmann, M., Hertel, C., Jilg, S., Tatzel, R., Zitzelaberger, H., Liebl, S., Hochberger, M., Shah, J., Lane, D. and Wallnoef, P.R. Complete 23S ribosomal RNA sequences of Gram-positive Bacteria with a low DNA G+C content alow DNA G+C content along the grant along the content along t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BCT 29-MAR-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PAT 17-JAN-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Euarchontoglires, Primates, Catarrhini;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                            Score 24.4; DB 15; Length 110000; Pred. No. 65;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BV11 bp DNA linear PAT 1 Primer for synthesizing full-length cDNA and use thereof. BD147349
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          238 ribosomal RNA.
Streptococcus oralis
Streptococcus oralis
Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
                                                                                                                                                                                                                                                                                                                                                  ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 60.0%; Score 24; DB 1; Length 2902; Best Local Similarity 84.4%; Pred. No. 1e+02; Matches 27; Conservative 0; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                  6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        linear
                                                                                                                                                                                                                                                                                                                                                                                                                                  17273 TCCAGATTCTTGGAAGTGGTGAGATACTTGGTCA 17306
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /organism="Streptococcus oralis"
/mol_type="genomic DNA"
/strain="DSM 20066"
/d_zeef="taxon:1303"
1. -2902
                                                                                                                                                                                                                                                                                                                                                                                                      2 TCCAGATTCTTGGCGGTAGAGAGCTGCTTGGTCA 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         876 ATCAAGATTCTTGGAGGTAGAGCACTGTTTGG 907
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 ATCCAGATTCTTGGCGGTAGAGAGCTGCTTGG 32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /product="23S ribosomal RNA"
                                                                                                                                                                                                                                                                                                                                                  0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2902 bp
                              2510000
2510000
2610000
2710000
2810000
3010000
          2310000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                S.oralis gene for 23S rRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BD147349.1 GI:27853107
JP 2002191363-A/2192.
Homo sapiens (human)
Homo sapiens
                                                                                                                                                                                                                                                                                            61.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    X68427.1 GI:288522
     2200001
2400001
2500001
2500001
2600001
2700001
2900001
                                                                                                                                                                                                                                                                                                                                                  28; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Streptococcus.
                                                                                                                                                                                                                                                                                                                       Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SO23SRRN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              X68427
     CR382128_22
CR382128_23
CR382128_24
CR382128_25
CR382128_26
CR382128_27
CR382128_27
CR382128_29
                                                                                                                                                                                                                                                                                                 Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 6
BD147349/c
LOCUS
DBFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DEPINITION
                                                                                                                                                                                                                                                                                                                                                  Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ACCESSION
VERSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REFERENCE
AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REFERENCE
AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TITLE
JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   rrna
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                KEYWORDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 5
SO23SRRN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LOCUS
```

. . . .

à

TITLE

COMMENT

```
eurbeil5 2343 bp DNA linear PAT 17-JAN-2003
Primer for synthesizing full-length cDNA and use thereof.
BD158115
                                                                                                                                                                                                                              Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini, Hominidae, Homo.

1 (bases 1 to 2343)
Ota,T., Isogai,T., Nishikawa,T., Hayashi,K., Saito,K., Yamamoto,J., Ishii,S., Sugiyama,T., Wakamatsu,A., Nagai,K. and Otsuki,T. Primar for synthesizing full-length cDNA and use thereof Patent: JP 2002191363-A 12958 09-UUL-2002;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PAT 17-DEC-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ota,T., Isogai,T., Nishikawa,T., Hayashi,K., Saito,K., Yamamoto,J., Ishii,S., Sugiyama,T., Wakamatsu,A., Nagai,K. and Otsuki,T. Primers for synthesising full-length cDNA and their use Patent: EP 1074617-A 14860 07-FEB-2001; Research Association for Biotechnology (JP)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          JUNICHI YAMAMOTO, SHIZUKO ISHII, TOMOYASU SUGIYAMA, AI WAKAMATSU,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C12N15/09, C07K14/47, C07K16/18, C12N1/15, C12N1/19, C12N1/21, C12N5/ PC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C C12P21/02,C12Q1/68//C12P21/08,G06F17/30,C12N1S/00,C12N5/00 CC Primer for synthesizing full-length cDNA and use thereof FH Key Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Buarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens (human)
JP 2002191363-A/12958
09-JUL-2000
09-JUL-2000 JP 2000280990
TOSHIO OTA, TAKAO ISOGAI, TETSUO NISHIKAWA, KOJI HAYASHI, KAORU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 2343;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 59.5%; Score 23.8; DB 6; Best Local Similarity 80.0%; Pred. No. 1.38+02; Matches 28; Conservative 0; Mismatches 7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 ATCCAGATTCTTGGCGGTAGAGAGCTGCTTGGTCA 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note="unnamed protein product"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2343 bp DNA Sequence 14860 from Patent EP1074617. AX879955
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (61). (2022).
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        KEIICHI NAGAI, TETSUJI OTSUKI
                                                                                                                  BD158115.1 GI:27863873
JP 2002191363-A/12958.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AX879955.1 GI:40034691
                                                                                                                                                                           Homo sapiens (human)
Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens (human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ното варіепв
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    S N G A I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               KEYWORDS
SOURCE
ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       source
                              LOCUS
DEFINITION
ACCESSION
                                                                                                               VERSION
KEYWORDS
SOURCE
ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AX879955/c
   3D158115/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ACCESSION
VERSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TITLE
JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                        JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AUTHORS
                                                                                                                                                                                                                                                                                                                        REFERENCE
                                                                                                                                                                                                                                                                                                                                                       AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PEATURES
                                                                                                                                                                                                                                                                                                                                                                                                             TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Locus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ઠ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   / LTAIN BLACK ON THE TOOL THE THE TOOL TO THE TOOL TO THE TOOL TO THE TOOL 
                                             HSAE05016 2126 bp mRNA linear PRI 31-OCT-2002
Homo sapiens mRNA for retinoblastoma-associated factor 600-like
protein (RBAF600 gene), mutant allele.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Lennerz,V.
Direct Submission
Direct Submission
Submitted OG-AUG-2002) Lennerz V., III. Medizinische Klinik,
Johannes Gutenberg-University of Mainz, Langenbeckstrasse 1, 55101
Mainz, GERWANY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Response of autologous T cells to a human melanoma is dominated by
                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
                                                                                                                                                AJ505016
AJ505016.1 GI:24474788
RBAF600 gene; retinoblastoma-associated factor 600-like protein.
Homo sapiens (human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                          Gentilini, C., Fatho, M., Lennerz, V., Lifke, A., Woelfel, C. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              'product="retinoblastoma-associated factor 600-like
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 2126;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 59.5%; Score 23.8; DB 8; 3
Best Local Similarity 80.0%; Pred. No. 1.3e+02;
Matches 28; Conservative 0; Mismatches 7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /protein_id="CAD43719.1"
/db_xref="G1:24474789"
/db_xref="UniProt/TrEMBL:Q8IXJ4"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        373 Arccaarrcrrececraecearerecrrrrea 339
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 ATCCAGATTCTTGGCGGTAGAGAGCTGCTTGGTCA 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         'evidence=experimental
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /sex="female"
/cell_line="MZ7-MEL"
/cell_type="melanoma"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /country="Germany"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 individual mutant antigens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /gene="RBAF600"
/replace="g"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      gene="RBAF600"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       41. .1807
/gene="RBAF600"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             'note="mutant"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (bases 1 to 2126)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               protein"
                                                                                                                                                                                                                                                                                                                                                       Hominidae, Homo.
                                                                                                                                                                                                                                                               Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                     Woelfel, T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        variation
RESULT 8
HSA505016/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bource
                                                         LOCUS
DEFINITION
                                                                                                                                                                                                                                                               ORGANISM
                                                                                                                                          ACCESSION
VERSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TITLE
JOURNAL
                                                                                                                                                                                                                                                                                                                                                                               REFERENCE
AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REFERENCE
AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            JOURNAL
                                                                                                                                                                                                   KEYWORDS
SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               σ
```

RESULT :

ઠ 셤

ORIGIN

ORIGIN

8 셤

```
Unpublished

State of the control of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Cranlata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.

Hominidae; Homo.

Joseph Homo.

Ota,T., Isogai,T., Nishikawa,T., Hayashi,K., Saito,K., Yamamoto,J., Ishii,S., Sugiyama,T., Wakamatsu,A., Nagai,K. and Otsuki,T. Primer for synthesizing full-length cDNA and use thereof Patent: JP 2002191363-A 10897 09-UUL-2002;

HELIX RESEARCH INSTITUTE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BD156054 2390 bp DNA linear PAT 17-JAN-2003 Primer for synthesizing full-length cDNA and use thereof. BD156054
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   JUNICHI YAMAMOTO, SHIZUKO ISHII, TOMOYASU SUGIYAMA, AI WAKAMATSU,
KRIICHI NAGAI, TETSUJI OTSUKI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C12N15/09, C07K14/47, C07K16/18, C12N1/15, C12N1/19, C12N1/21, C12N5/ PC
                                      Isogai, T., Ota, T., Hayashi, K., Sugiyama, T., Otsuki, T., Suzuki, Y., Nishikawa, T., Nagai, K., Sugano, S., Takahashi-Fujii, A., Hara, H., Tanase, T., Nomura, Y., Togiya, S., Komai, F., Hara, R., Takeuchi, K., Arita, M., Nabekura, T., Ishii, S., Kawai, Y., Saito, K., Yamamoto, J., Wakamatsu, A., Nakamura, Y., Nagahari, K., Masuho, Y. and Oshima, A. NEDO human cDNA sequencing project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOSHIO OTA, TAKAO ISOGAI, TETSUO NISHIKAWA, KOJI HAYASHI, KAORU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         mRNA from NT2 neuronal precursor cells after 2-weeks retinoic acid (RA) induction."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 2343;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note="cloning vector: pME18SFL3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Match 59.5%; Score 23.8; DB 8; Local Similarity 80.0%; Pred. No. 1.3e+02; tes 28; Conservative 0; Mismatches 7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  591 Arccaarrcrrddddraraddargrarrrca 557
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 ATCCAGATTCTTGGCGGTAGAGAGCTGCTTGGTCA 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      type="teratocarcinoma"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1. .2343
/organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /mol_type="mRNA"
/db_xref="taxon:9606"
/clone="NT2RP2003567"
/cell_line="NT2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              09-JUL-2002
28-JUL-2000 JP 2000280990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens (human)
JP 2002191363-A/10897
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BD156054.1 GI:27861812
JP 2002191363-A/10897.
Homo sapiens (human)
Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bource
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BD156054/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LOCUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                   AUTHORS
TITLE
JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Loc
Matches
REFERENCE
AUTHORS
                                                                                                                                                                                                                                                                                TITLE
JOURNAL
REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         VERSION
KEYWORDS
SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DRIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            요
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ota,T., Suzuki,Y., Nishikawa,T., Otsuki,T., Sugiyama,T., Irie,R., Wakamatsu,A., Hayashi,K., Sato,H., Nagai,K., Kimura,K., Makita,H., Sakine,M., Obayashi,M., Nishi,T., Shibahara,T., Tanaka,T., Ishibahara,T., Tanaka,T., Ishibahara,T., Tanaka,T., Ishibi,S., Yamamoto,J., Saito,K., Kawai,Y., Isono,Y., Nakamana,Y., Nagatsuma,M., Sudahari,K., Yadanda,T., Tavaka,Y., Kodaira,H., Kondo,H., Sudo,H., Hosoiri,T., Kakuy,Y., Kodaira,H., Kondo,H., Shiratori,A., Sudo,H., Hosoiri,T., Yakuy,Y., Kotsuta,N., Sato,K., Tanai,M., Yamazaki,M., Ninomiya,K., Ishibashi,T., Yamashita,H., Kimata,M., Watanabe,M., Hiraoka,S., Culba,Y., Tanai,H., Kimata,M., Watanabe,M., Hara,H., Tanase,T., Nomura,Y., Togiya,S., Komai,F., Hara,R., Tanaka,M., Imose,N., Musashino,K., Yuuki,H., Oshima,A., Sasaki,M., Arita,M., Imose,N., Wasashino,K., Yuuki,H., Oshima,A., Sasaki,N., Saro,S., Woriya,S., Momiyama,H., Satoh,N., Takani,S., Moriya,S., Momiyama,H., Nimada,H., Watanabe,T., Shiohata,N., Sano,S., Moriya,S., Senoh,A., Mizoguchi,H., Tanaka,Y., Suzuki,O., Nakagawa,S., Senoh,A., Mizoguchi,H., Tanaki,A., Takemoto,M., Kawakami,B., Yamazaki,M., Watanabe,T., Sugiyama,A., Takemoto,M., Kawakami,B., Yamazaki,M., Watanabe,T., Noguchi,A., Hishigaki,H., Nakanaba,M., Matanabe,T., Namagai,A., Takema,Y., Senba,A., Hikiji,T., Kobatake,N., Tashiro,H., Tanigami,A., Puliyara,T., Ono,T., Yamada,K., Pulii,Y., Tashiro,H., Tanigami,A., Puliyara,T., Ono,T., Yamada,K., Pulii,Y., Nakajima,Y., Suzuki,O., Nakayama,B., Hikiji,T., Kobatake,N., Nakajima,Y., Mizuno,T., Morinaga,M., Sabaki,M., Togashi,T., Nakanube,M., Kawakami,T., Matanabe,M., Satoh,T., Shigtes,M., Sanaki,M., Togashi,T., Nakanube,M., Sasaki,M., Togashi,T., Shirai,Y., Takabashi,Y., Nakaubo,Y., Yamadi,R., Yada,T., Nakamura,Y., Ohara,O., Isogai,T. and Sugano,J., Nakai,K., Yada,T., Nakamura,Y., Ohara,O., Isogai,T. and Sugano,S., Nakai,K., Yada,T., Nakamura,Y., Ohara,O., Isogai,T., Nakanura,Y., Ohara,O., Isogai,T., Nakanura,Y., Ohara,O., Isogai,T., Nakanupa,M., Sulani,M., Mara,M., Mara,M., Mara,M., Mara,M., Mara,M., Mara,M., Mara,
                                                                                                                                                                     ALEGIBLE SERVICTORIA TO THE THEORY OF THE TH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2343 bp mRNA linear PRI 30-JAN-2004 Homo sapiens cDNA FLJ12862 fis, clone NT2RP2003567, highly similar to Homo sapiens mRNA for KIAA0462 protein.
    /codon_start=1
/proteIn_id="CAB90737.1"
/db_xref="G1:#003462"
/translation="MNTLNVMLGTLNLALVAEQESKOSGGAAVAEQVLSIMBIILDES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Buarchontoglires, Primates, Catarrhini,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 59.5%; Score 23.8; DB 6; Length 2343; Best Local Similarity 80.0%; Pred. No. 1.3e+02; Matches 28; Conservative 0; Mismatches 7; Indels 0.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AK022924
AK022924.1 GI:10434594
oligo capping; fis (full insert sequence).
Homo sapiens (human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         591 ATCCAAATTCTTGGCGCTAGGGATGTGCTTTTTCA 557
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 ATCCAGATICTIGGCGGTAGAGAGCTGCTTGGTCA 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      human cDNAs
Nat. Genet. 36 (1), 40-45 (2004)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Nat. Gene
14702039
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LOCUS
DEPINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AK022924/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        VERSION
KEYWORDS
SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PUBMED
```

TITLE

ö

Gaps ö

FEATURES

ORIGIN

```
Ota, T., Suzuki, Y., Nishikawa, T., Otsuki, T., Sugiyama, T., Irie, R., Wakamatsu, A., Hayashi, K., Sato, H., Nagai, K., Kimura, K., Makita, H., Shibahara, T., Tanaka, T., Ishibahara, T., Tanaka, T., Ishibahara, T., Tanaka, T., Ishibahara, T., Tanaka, T., Ishii, S., Yamamoto, J., Saito, K., Kawai, Y., Isono, Y., Nakamura, Y., Nagahari, K., Murakami, K., Yasuda, T., Kawai, Y., Kodaira, H., Kondo, H., Sugawara, M., Takahashi, M., Ninomiya, Y., Kodaira, H., Kondo, H., Sugawara, M., Takahashi, M., Ninomiya, K., Katsuta, N., Sato, K., Kikkawa, E., Culba, Y., Ishida, S., Ono, Y., Takiguchi, S., Watanabe, M., Hiraoka, S., Chiba, Y., Ishida, S., Ono, Y., Takiguchi, F., Watanabe, M., Haraoka, M., Hotuta, T., Kusano, J., Kanehori, R., Watanabe, M., Haraoka, M., Hotuta, T., Nomura, Y., Togiya, S., Komai, F., Hara, R., Takeuchi, K., Arita, M., Imose, N., Musashino, K., Yuuki, H., Oshima, A., Sasaki, N., Arita, M., Imose, N., Musashino, K., Yuuki, H., Oshima, A., Sasaki, N., Arita, M., Imose, N., Musashino, K., Yuuki, H., Oshima, A., Sano, S., Moriya, S., Momiyama, H., Ishihara, T., Shiohata, N., Sano, S., Moriya, S., Momiyama, H., Ishihara, T., Shiohata, V., Shinizu, F., Wakebe, H., Hishigaki, H., Watanabe, K., Kumagai, A., Itakura, S., Fukuzumi, Y., Fujimori, Y., Kawakami, T., Kawakami, T., Kawakami, T., Moguchi, H., Matanaba, A., Hikiji, T., Kobatake, N., Inagaki, H., Ikana, Y., Matanabe, M., Komatsu, Y., Matanabe, M., Komatsu, Y., Matanabe, M., Sanda, M., Sasaki, M., Satoh, M., Sasaki, M., Satoh, M., Sasaki, M., Satoh, M., Sanda, M., Satoh, M., Nakai, Y., Nakamura, Y.
"O sapiens cDNA FLJ10371 fis, clone NT2RM2001903, highly similar Homo sapiens mRNA for KIAA0462 protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Genomics Laboratory; 1532-3 Yana, Kisarazu, Chiba 292-0812, Japan (B-mail:genomics@hri.co.jp, Tel:81-438-52-3975, Fax:81-438-52-3986) NEDO bhuman cDNA sequencing project supported by Ministry of International Trade and Industry of Japan, cDNA full innert sequencing: Research Association for Biotechnology; cDNA library construction, 5'- & 3'-end one pass sequencing and clone selection: Helix Research Institute (supported by Japan Key Technology Center etc.) and Department of Virology, Institute of Medical Science, University of Tokyo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Isogai, T., Ota, T., Hayashi, K., Sugiyama, T., Otsuki, T., Suzuki, Y., Nishikawa, T., Nagai, K., Sugano, S., Shiratori, A., Sudo, H., Wagatsuma, M., Hosoiri, T., Kaku, Y., Kodaira, H., Kondo, H., Sugawara, M., Takahashi, M., Chiba, Y., Ishida, S., Murakawa, K., Ono, Y., Takiguchi, S., Watanabe, S., Kimura, K., Murakami, K., Nahii, S., Kawai, Y., Saito, K., Yamamoto, J., Wakamatsu, A., Nagahari, K., Masuho, Y., Ninomiya, K. and Iwayanagi, T. Nabo, human cDNA sequencing project
                                                                                                                                                                                                                                                                                                                   Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Buarchontoglires, Primates, Catarrhini;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Unpublished

3 (Dases 1 to 2390)

18ogai,T. and Otsuki,T.

Direct Submission
Submitted (16-FEB-2000) Takao Isogai, Helix Research Institute,
                                                                                                                                                                                                          oligo capping; fis (full insert sequence)
Homo sapiens (human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /organisme"Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Nat. Genet. 36 (1), 40-45 (2004)
14702039
                                                                    Homo sapiens cDNA FLJ10371 fis,
                                                                                                                                                                             AK001233.1 GI:7022359
                                                                                                                                                                                                                                                                                                                                                                                           Hominidae; Homo.
                                                                                                                                                                                                                                                                                      Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    human cDNAs
                                                                                                                                                                         VERSION
KEYWORDS
SOURCE
ORGANISM
                                                                        DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PUBMED
REFERENCE
AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TITLE
JOURNAL
REFERENCE
AUTHORS
TITLE
JOURNAL
                                                                                                                                         ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                            REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LHKLEQVSSDEGIGTLAENLLEALREHPDVNKKIDAARRETRAEKKRMAMANRQKALG
TLGWTTNEKGQVVTKTALLKQMEBLIEBFGIFTCICREGYKROPTKVLGIYTFTRNV
LEBLENKRPRKOGGYSTVSHPIVHYDCHLAAVRLARGREEWESAALGNANTKCNGLLB
VWGBHVPESARATCIARHNYLQECTGGREEYYQLAIHDIKLLFLERAMGSESADTG
GGGRESNIHLIPYLYVLANTRATSREEKNLQGFLEQPKGKWVESAFEVDGPYY
TYLALHIIPPEQWATRYBLIRRLLYTSQARAMGGGFLEQPKGKWVESAFEVDGPYY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ota,T., Isogai,T., Nishikawa,T., Hayashi,K., Saito,K., Yamamoto,J., Ishii,S., Sugiyama,T., Wakamatsu,A., Nagai,K. and Otsuki,T. Primers for synthesising full-length cDNA and their use Patent: BP 1074617-A 11199 07-FBB-2001; Research Association for Biotechnology (JP)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PAT 17-DEC-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /trānglation="mytlnymlgtlnlalvaegeskosggaavarqvlliddes
naeplsedkgnllligdkoolvmlldgingtfvrsnpsvloggllriipylsfgevekm
Qilverfkpycnfdkydedhsgddkvfldcfckiaagiknnsnghqlkolilqkgitq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FWALVDLIYNMFKKVPTSNTEGGWSCSLAĒYIRHNDMPIYEAADKALKTPQEBFMPVB
TFSEFLDVAGLLSBITDPESFLKDLLNSVP"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NALDYMKKHI PSAKNLDADIWKKFLSRPALPFILRLLRGLAIQHPGTQVLIGTDSIPN
                                    C12P21/02, C12Q1/68//C12P21/08, G06F17/30, C12N15/00, C12N5/00 CC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Buarchontoglires, Primates, Catarrhini,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                PC C12P21/02,C12Q1/68//C12P21/04,GUDE1/1-0,C12C1/05/PTIMER for synthesizing full-length CDNA and use thereof FH Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                                        Score 23.8; DB 6; Length 2390;
Pred. No. 1.3e+02;
0; Mismatches 7; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        59.5%; Score 23.8; DB 6; Length 2390; 80.0%; Pred. No. 1.3e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pred. No. 1.3e+02;
0; Mismatches 7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      649 Arccaarrcrrccccraccarcrcrrrrca 615
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 ATCCAGATTCTTGGCGGTAGAGAGCTGCTTGGTCA 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 ATCCAGATTCTTGGCGGTAGAGAGCTGCTTGGTCA 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        'note="unnamed protein product"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2390 bp DNA
Sequence 11199 from Patent EP1074617.
AX876294
                                                                                                                                         (119). .(2080).
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
119-.2083
                                                                                                                                                                                                              1. .2390
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /protein id="CAE89207.1"
/db_xref="GI:40031031"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AX876294.1 GI:40031030
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                        ch 59.5%;
1 Similarity 80.0%;
28; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens (human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best Local Similarity 80.0
Matches 28; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
Matches 28; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
```

source

PEATURES

TITLE JOURNAL

REFERENCE AUTHORS RESULT 14 AK001233/c

ઠ 셤

RESULT 13
AX876294/c
LOCUS
DEFINITION
ACCESSION
VERSION

셤

ORGANISM

KEYWORDS SOURCE

```
셤
           ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PC C12N15/06, A61K38/00, A61K45/00, A61P1/16, A61P5/06 PC
A61P5/14, A61P7/00,
PC A61P7/00, A61P11/00, A61P11/06, A61P13/12, PC
A61P15/00
PC A61P17/00, A61P19/00, A61P19/08, A61P21/00, A61P21/04, A61P25/00,
PC A61P27/12,
A61P27/12,
A61P27/12,
A61P27/12,
A61P27/12,
A61P27/12,
A61P27/18,
PC A61P27/18,
PC A61P37/08,
A61P37/08,
A61P37/08, A61P35/00, A61P35/02, A61P37/00, A61P31/12,
PC A61P37/18,
PC COTK14/47,
PC COTK14/48, C12N1/15, C12N1/19, C12N1/21, C12N5/10, C12P21/02 PC
C12Q1/68, G01N33/53,
PC G1N33/56, G10N33/50, (C12P21/02, C12R1:91), (C12P21/
PC C12N15/00, C12N5/00, A61K37/02
PC C12N15/00, C12N15/00, A61K37/02
PC C12N15/00, C12N15/00, A61K37/02
PC C12N15/00, C12N15/00, A61K37/02
PC T1CYTE Clone No: 1849911
FR Key

In Cacation/Qualifiers
FT Source

// Organism='Homo sapiens (human)'.
                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                     PAT 17-JUL-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Buarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
1 (bases 1 to 2650)
Tang,T.Y., Corley,N.C., Baughn,M.R., Reddy,R., Guegler,K.J. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DNA replication- and repair-associated proteins
Patent: JP 2002525032-A 3 13-AUG-2002;
INCYTE PHARMACUTICLALS INC
OS Homo sapiens (Innam)
PN JP 2002525032-A/3
PD 13-AUG-1999 JP 2000563781
PR 07-AUG-1999 US 60/155245,27-AUG-1998 US 60/155181 PI
TOM Y TANG,NBIL C CORLEY, MARIAH R BAUGHN, ROOPA REDDY, KARL J PI
                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
/clone="NT2RM2001903"
/cell_line="NT2"
/cell_type="teratccarcinoma"
/clone_lib="NT2RM2"
/note="Cloning vector: pME18SFL3
mRNA from uninduced NT2 neuronal precursor cells."
                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 59.5%; Score 23.8; DB 6; Length 2650; Best Local Similarity 80.0%; Pred. No. 1.3e+02; Matches 28; Conservative 0; Mismatches 7; Indels 0
                                                                                                                                                                                     Length 2390;
                                                                                                                                                                                                                                                                                                                                                                                                                                     linear
                                                                                                                                                                                                                               7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                         2650 bp DNA linea DNA separated proteins. BD249583.1 GI:33059353 JP 2002525032-A/3. Homo sapiens (human)
                                                                                                                                                                                59.5%; Score 23.8; DB 8;
80.0%; Pred. No. 1.3e+02;
iive 0; Mismatches 7;
                                                                                                                                                                                                                                                                                                                     649 Arccaaarrcrregeecraegearerecrrrrea 615
                                                                                                                                                                                                                                                                           1 ATCCAGATTCTTGGCGGTAGAGAGCTGCTTGGTCA 35

    .2650
    /organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Location/Qualifiers
                                                                                                                                                                                                                             28; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         HENRY YUE
                                                                                                                                                                                                   Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GUEGLER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Yue, H.
                                                                                                                                                                                     Query Match
                                                                                                                                                                                                                                                                                                                                                                                    RESULT 15
BD24583/c
LOCUS
DEFINITION
ACCESSION
VERSION
VERSION
SOURCE
ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           source
                                                                                                                                                                                                                               Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REFERENCE
AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TITLE
JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMMENT
                                                                                                                                         ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ORIGIN
                                                                                                                                                                                                                                                                                                                   셤
                                                                                                                                                                                                                                                                           ઠ
```

This Page Blank (uspto)

Ade40129 Human NOV Adr83456 Human ret

Adx06153 Cyclin-de Add85710 Baccerial Adb07057 Alloiococ Continuation (3 of Aah66350 C glutam Aah66350 C glutam Add13935 C glutam Add13935 C glutam Add13935 C glutam Aah68528 C glutami Aah6852 C glutami Aah6852 C glutami Aah635616 Probe #24 Aak23597 Human foe Aak23591 Human foe Aak23591 Human foe Aak23591 Human foe Aak40371 Human liv Aba62561 Human foe Aak62561 Human foe

Abs36435 Human liv Abs10777 Human gen Adx25701 Novel cel Adx26166 Novel cel

```
toxic effect; gene expression profile; hepatotoxicity; diagnostic marker; toxicity marker; toxicity progression; drug screening; primary rat hepatocyte toxicity modelling; gene; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                Primary rat hepatocyte toxicity modelling related gene SEQ ID NO:1103.
                                                                                                                                                                                                                                                                                                         ALIGNMENTS
                    ADX06153
ADS45710
ADB07057
ADB07055
ADB12064_02
AAH66350
ACA00491
                                                                                               AEB15386
ADD13935
AAL46365
                                                                                                                                                                                                                                                               ADX25701
ADX26166
                                                                                                                                             AAD59410
                                                                                                                                                                          AAK23597
ABS49351
ABS23215
ABA62561
AAI42547
AAK10917
                                                                                                                                                                                                                                         ABS36435
                                                                                                                                AAH68528
                                                                                                                                                      ABA75082
                                                                                                                                                                                                                                                     ABS10777
                                                                                                                                                                                                                                                                                                                                          RESULT 1
ADB50561/c
ID ADB50561 standard; DNA; 456 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2002US-0370246P.
2002US-0371134P.
2002US-0371135P.
2002US-0371413P.
2002US-0373601P.
2002US-0373602P.
2002US-0374139P.
2002US-0374139P.
2002US-0378370P.
2002US-0378370P.
2002US-0378370P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2002US-0353171P.
2002US-0363534P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2003WO-US003482
 04-DEC-2003 (first entry)
                                                                                                                                                     262
262
262
262
262
572
572
572
572
572
572
572
9508
15552
15552
1266
110000
1107
1164
1234
1234
349980
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Rattus norvegicus.
 WO2003065993-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          08-APR-2002; 210-APR-2002; 210-APR-2002; 2110-APR-2002; 211-APR-2002; 19-APR-2002; 219-APR-2002; 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 04-FEB-2003;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            14-AUG-2003
 23.8
23.8
23.6
23.6
23.8
23.8
                                                                           ADB50561;
  Adh50561 Primary r
Adh54859 Rat insul
Adh54925 Rat insul
Abk36163 cDNA segu
Aah05357 Human cDN
Aah16123 Human cDN
Aah14062 Human cDN
Aa23150 Seguence
Aac33150 Seguence
Aac3410 Human cDN
Abg54736 Human cDN
Abg54736 Human cDN
Aca56981 Human cDN
Aca56881 Human cDN
                                                                          April 18, 2006, 19:05:32 ; Search time 219 Seconds (without alignments) 1217.295 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Description
           5.1.7
Biocceleration Ltd.
                                                                                                                                                                                                                      9993994
                                                                                                                                            1 atccagattcttggcggtagagagctgcttggtcagactt
                                                                                                                                                                                                                     Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                4996997 segs, 3332346308 residues
            GenCore version
Copyright (c) 1993 - 2006
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SUMMARIES
                                                                                                                                                                                                                                                                           Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                      nucleic search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADB50561
ADH54925
ADH54925
ABK36163
ABK36163
ABK36179
AAH16123
AAC93150
AAC93150
AAC93410
AAC93410
                                                                                                                                                                IDENTITY_NUC
Gapop 10.0 , Gapext 0.1
                                                                                                                                                                                                                                                                                                                     Geneseq.21:*

geneseqn1980s:*
geneseqn200s:*
geneseqn2001s:*
geneseqn2001bs:*
geneseqn2001bs:*
geneseqn2002bs:*
geneseqn2003bs:*
                                                                                                                                                                                                                                                                                                                                                                                                                                  geneseqn2003cs:*
geneseqn2003ds:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                      geneseqn2004as:*
geneseqn2004bs:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              geneseqn2005s:*
                                                                                                                                                                                                                                             seq length: 0
seq length: 200000000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query
Match Length DB
                                                                                                                       SEQ4 - THEN - SEQ3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1640
860
861
871
2343
22343
2243
22550
22770
22650
22770
77228
77228
77228
77228
77228
77228
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Title:
Perfect score:
                                                                                                                                                                Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score
                                                                                                                                                                                                                                            Minimum DB
Maximum DB
                                                      OM nucleic
                                                                                                                                             Sequence:
                                                                                                                                                                                                   Searched:
                                                                                                                                                                                                                                                                                                                        Database
                                                                            Run on:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Result
```

2002US-0394230P. 2002US-0394253P. 2002US-0407688P. 2003US-0442900P.

22-APR-2002; 08-MAY-2002; 09-MAY-2002; 09-MAY-2002;

09-MAY-2002; 09-JUL-2002; GENE LOGIC INC

(GENE-)

ADQ98434 ADB48194 ADF81716

ACA56981 AAS44988

0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0

υ

28-JAN-2003;

for drug screening or diagnostic indicator for the loss of glucose-

English.

Claim 1; SEQ ID NO 1; 93pp;

cell, for

responsiveness.

Orr M;

Castle A,

```
The present invention describes a method for determining whether a compound induces a toxic effect on a tissue or cell. The method comprises preparing a gene expression profile of a tissue or cell sample exposed to the compound, and comparing the gene expression profile to a database comprising data or information on the Tox mean and non-Tox mean value. The method is useful for predicting or identifying at least one toxic effect, particularly hepatotoxicity, of a test or unknown compound. The genes listed in the specification are useful as diagnostic or toxicity markers for the prediction or identification of the physiological state of tissue or cell sample that has been exposed to a compound, or to identify or predict the toxic effects of a compound or an agent. These may also be used as markers for monitoring toxicity progression or for drug screening. The present sequence represents a primary rat hepatocyte toxicity modelling related gene sequence from the present invention.
                                                                                                                                                                                                        Determining if a compound induces a toxic effect on a tissue or cell, for identifying hepatotoxic compounds, comprises comparing a gene expression profile of a tissue or cell sample to a database of Tox mean and non-Tox
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Rat; insulinoma differentially expressed clone; ss; glucose response;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 456 BP; 123 A; 95 C; 103 G; 135 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         369 Arccrearrerrecearadacaacacerreceacacr 331
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 ATCCAGATTCTTGGCGGTAGAGAGCTGCTTGGTCAGACT 39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Rat insulinoma differentially expressed clone 8.
                                Higgs B,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     4.6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 76.9%; Pred. No. 4.º
Matches 30; Conservative 0; Mismatche
                                                                                                                                                                                                                                                                                                                                                                                       Claim 44; SEQ ID NO 1103; 874pp; English
                                    Johnson K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADH54859 standard; cDNA; 1105 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         19-FEB-2002; 2002US-00080381.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (first entry)
                                    Porter M,
                                                                                                                                   WPI; 2003-731472/69.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       insulin; diabetes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US2003148421-A1
                                Mendrick D,
Elashoff M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               25-MAR-2004
                                                                                                                                                                                                                                                                                                                  mean values.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       07-AUG-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Rattus sp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADH54859;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 2
ADH54859
ID ADH5,
XX
AC ADH5,
XX
DT 25-M
XX
KW RAL;
KW INBU
XX
COS RACC
COS
Š
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      셤
```

20-FEB-2001; 2001US-0270251P. 09-MAR-2001; 2001US-0274706P. 15-MAY-2001; 2001US-0291354P.

Jensen PB;

Newgard CB,

WPI; 2003-897569/82.

(NEWG/) NEWGARD C B. (JENS/) JENSEN P B.

Indels

6

```
The invention relates to an isolated polymucleotide (differentially expressed by Insulinoma cells) encoding a protein involved in regulating expressed by Insulinoma cells) encoding a protein involved in regulating clauses responses. Also included are an expression cassette (comprising the polymucleotide and a promoter, where the polymucleotide is positioned to oil gonucleotide of 15-50 bases (comprising 15 or more bases of polymucleotide encoding the polymptide, a method of expressing a polymucleotide, a polypeptide comprising the heterologous polymucleotide, a polypeptide comprising a sequence encoded by the polymptide of 5-15 residues comprising 5 or more consecutive residues of the polypeptide, a monoclonal antibody that binds immunologically to the polypeptide, a mucleic acid encoding the antibody, composition, where the antibodies bind immunologically to the polypeptide, a method for medulating the glucoseresponsiveness of a cell, a method of screening for a modulator of the polypeptide and a method for measuring the expression of the polypeptide and a method for measuring the consecutive in the polypeptide and a method for measuring the cell that secrets insulfn, and as target for drug screening or diagnostic indicator for the loss of glucose-responsiveness in a host cell that secrets insulfn, and as target for drug screening or diagnostic indicator for the loss of glucose-responsiveness en in diabbetes. The present sequence is an isolated polymucleotide (differentially expressed by the polymptide and protein involved in regulating glucose
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Rat; insulinoma differentially expressed clone; ss; glucose response;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New polynucleotide, useful for enhancing, stabilizing or introducing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 1105;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Rat insulinoma differentially expressed clone 8 3' sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 1105 BP; 286 A; 266 C; 255 G; 297 T; 0 U; 1 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  742 ATCCTGATTCTTGCCGATAGACAACAGCTTGCCCACACT 780
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 ATCCAGATTCTTGGCGGTAGAGAGCTGCTTGGTCAGACT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61.5%; Score 24.6; DE 76.9%; Pred. No. 5.5; ive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADH54925 standard; cDNA; 1640 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      19-FEB-2002; 2002US-00080381.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             20-FEB-2001; 2001US-0270251P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             09-MAR-2001; 2001US-0274706P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   responses of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity 76.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Jensen PB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (NEWG/) NEWGARD C B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2003-897569/82.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             JENSEN P B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             insulin; diabetes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US2003148421-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              25-MAR-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Newgard CB,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               07-AUG-2003.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Rattus sp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADH54925;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (JENS/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADH54925
#X#X#X#X###X#X#X#X
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ઠ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New polynucleotide, useful for enhancing, stabilizing or introducing glucose-responsiveness in a host cell that secrets insulin, or as target
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 10; Length 456;
```

ö

Gaps

WPI; 2002-179322/23.

or as target

```
The invention relates to an isolated polynucleotide (differentially expressed by Insulinoma cells) encoding a protein involved in regulating expressed by Insulinoma cells) encoding a protein involved in regulating to the polynucleotide and a promoter, where the polynucleotide is positioned to as to be under the regulatory control of the promoter), an oligonucleotide of 15-50 bases (comprising 15 or more bases of polynucleotide encoding the polynucleotide encoding the polypeptide, a method of expressing a polypeptide, a peptide of 5-35 residues comprising 5 or more polynucleotide, a peptide of 5-35 residues comprising 5 or more polynucleotide, a peptide of 5-35 residues comprising 6 or more polynucleotide, a polypeptide, a mucleic acid encoding the antibody immunologically to the polypeptide, a mucleic acid encoding the antibody immunologically to the polypeptide, a method for measuring the expression of the polypeptide and a method for measuring the expression of the polypeptide and a method for measuring the expression of the polypeptide and a method for measuring the contract of stabilising or introducing glucose-responsiveness in a host cell that secrets insulfn, and as target for drug screening or diagnostic indicator for the loss of glucose-responsiveness in a host cell that sequence is a 5 or 3 sequence fragment of an isolated polymucleotide (differentially expressed by insulinoma cells) encoding a protein
glucose-responsiveness in a host cell that secrets insulin, or as for drug screening or diagnostic indicator for the loss of glucose
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    involved in regulating glucose responses.
                                                                                                                 Claim 1; SEQ ID NO 67; 93pp; English
                                                              responsiveness.
```

Gaps ö DB 10; Length 1640; Sequence 1640 BP; 388 A; 404 C; 365 G; 472 T; 0 U; 11 Other; 9; Indels 0; Mismatches Score 24.6; Pred. No. 6: Pred. 61.5%; Local Similarity 76.9 tes 30; Conservative Query Match Best Local & Matches

ö

1277 Arccrearrerreccearacacacacerrecceacer 1315 1 ATCCAGATTCTTGGCGGTAGAGAGCTGCTTGGTCAGACT

ઠે 셤

ABK36163 standard; cDNA; 860 BP ABK36163; 

08-MAY-2002 (first entry)

cDNA sequence #554 encoding novel human secreted protein.

Human secreted protein, hyperproliferative disorder, autoimmune disorder, immune deficiency disorder; blood disorder; inflammatory disorder; inflammatory disorder; infectious disorder; allergic condition; neurodegenerative disorder; liver fibrosis; coagulation disorder; gene therapy; antimicrobial; tumour; cancer; hepatotropic; immunosuppressive; antirheumatic; gene; ss.

Homo sapiens

WO200177289-A2

18-OCT-2001

29-MAR-2001; 2001WO-US010232.

06-APR-2000; 2000US-0195605P.

(GEMY ) GENETICS INST INC.

Collins-Racie LA, Evans C; Bowman MR, Spaulding V, Wong GG; senick RJ, Gulukota K, Graham JR; Resnick RJ, Lavallie ER, Agostino MJ, Howes SH, Re Merberg D, Treacy M, Clark HF, Fechtel K, Mccoy JM, Jacobs K,

```
The present invention relates to the isolation of novel cDNA sequences which encode human secreted proteins. The cDNA sequences have been derived from a variety of human tissues. The invention also provides a method for producing proteins from these polymuclectide sequences. The proteins are useful for identifying compounds that modulate their activity and production. The sequences of the invention are useful for treating diseases such as hyperproliferative disorders (e.g. cancer), immune deficiency disorders (e.g. multiple sclerosis), blood disorders (e.g. thrombocytopaenia), inflammatory disorders (e.g. arthritis), infectious disorders (e.g. multiple sclerosis), blood disorders (e.g. precedents), altergic conditions (e.g. asthma), neurodegenerative disorders (e.g. Alzheimer's disease), liver fibrosis, coagulation disorders (e.g. Alzheimer's disease), liver fibrosis, sequences of the invention are also useful in gene therapy. ABK3610-captesent the cDNA sequences of the invention that encode for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                       variety of
for treating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                     Six hundred and twenty three polynucleotides derived from a variety human tissue sources which encode secreted proteins, useful for tree immune deficiencies and disorders such as autoimmune disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 23.8; DB 6; Length 860;
Pred. No. 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 860 BP; 225 A; 236 C; 240 G; 159 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     55 Arccaatriciriciciocriaggargiocrirrica
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 ATCCAGATTCTTGGCGGTAGAGAGCTGCTTGGTCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Mismatches
                                                                                                                               Claim 1; Page 362; 393pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  novel human secreted proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     59.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity 80.0
hes 28; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Loca
Matches
셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                8
```

Human; primer; detection; diagnosis; antisense therapy; gene therapy; ss. Human cDNA clone (5'-primer) SEQ ID NO:2192. 29-JUL-1999; 99JP-00248036. 27-AuG-1999; 99JP-00300253. 11-JAN-2200; 2000JP-00118776. 02-MAX-2000; 2000JP-00183767. 09-JUN-2000; 2000JP-00241899. 28-JUL-2000; 2000EP-00116126. AAH05357 standard; cDNA; 871 (first entry) Ното варіелв. EP1074617-A2. 07-FEB-2001. 26-JUN-2001 AAH05357; RESULT 5 AAH05357/c 

Yamamoto J; Saito K, , Otsuki Isogai T, Nishikawa T, Hayashi K, S Sugiyama T, Wakamatsu A, Nagai K, (HELI-) HELIX RES INST. shii S, Ota T.

Primer sets for synthesizing polymucleotides, particularly the 5602 full-length cDNAs defined in the specification, and for the detection and/or diagnosis of the abnormality of the proteins encoded by the full-length cDNAs.

WPI; 2001-318749/34.

```
The present invention describes primer sets for synthesising 5602 full-
length cDNAs defined in the specification. Where a primer set comprises:

(a) an oligo-dr primer and an oligonucleotide complementary to the complementary strand of a polynucleotide which comprises one of the 5602 nucleotide sequences defined in the specification, where the oligonucleotide comprises at least 15 nucleotides; or (b) a combination of an oligonucleotide comprising a sequence complementary to the complementary strand of a polynucleotide which comprises a 3'-end sequence complementary to the complementary strand of a polynucleotide which comprises a 3'-end sequence complementary to a polynucleotide which comprises a 3'-end sequence complementary to a polynucleotide which comprises a 3'-end sequence of the complementary to a polynucleotide which comprises a 1'-end sequence, where the oligonucleotide which comprises a 1'-end sequence of and the complementary full-length cDNAs. The primers are also useful for the specification. The primers are useful for synthesising polynucleotides, particularly full-length cDNAs. The primers are also useful for the cetection and/or diagnosis of the abnormality of the proteins encoded by the full-length cDNAs. The primers allow obtaining of the full-length cDNAs easily without any specialised methods. AAH0362 to AAH13628 and AAH13613 to PAH13612 represent human amino acid sequences; and AAH0362 to AAH13622 represent human amino acid sequences; and AAH0362 to AAH0362 represent complementary and the exemplification of the
                              Claim 1; SEQ ID NO 2192; 2537pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         present invention
```

ö Score 23.8; DB 4; Length 871; Pred. No. 11; 0; Mismatches 7; Indels Sequence 871 BP; 234 A; 220 C; 220 G; 194 T; 0 U; 3 Other; 1 ATCCAGATTCTTGGCGGTAGAGAGCTGCTTGGTCA 35 59.5%; Query Match
Best Local Similarity 80.00,

649 Arccaaarrerregeerragegargeerrrrea 615

ò 유 ABK36179 standard; cDNA; 1928 BP

ABK36179;

08-MAY-2002 (first entry)

cDNA sequence #570 encoding novel human secreted protein.

Human secreted protein; hyperproliferative disorder; autoimmune disorder; immune deficiency disorder; blood disorder; inflammatory disorder; infectious disorder; allergic condition; neurodegenerative disorder; liver fibrosis; coagulation disorder; gene therapy; antimicrobial; tumour; cancer; hepatotropic; immunosuppressive; antirheumatic; gene; ss. 

Homo sapiens

WO200177289-A2

18-OCT-2001.

06-APR-2000; 2000US-0195605P.

29-MAR-2001; 2001WO-US010232.

(GEMY ) GENETICS INST INC.

. Collins-Racie LA, Evans C; I, Bowman MR, Spaulding V, Wong GG; Resnick RJ, Gulukota K, Graham JR; Agostino MJ, Howes SH, R Lavallie ER, Treacy M, Fechtel K, Jacobs K, Mccoy JM, Merberg D, Clark HF,

Six hundred and twenty three polynucleotides derived from a variety of human tissue sources which encode secreted proteins, useful for treating

WPI; 2002-179322/23.

which encode human secreted proteins. The convention also provides a derived from a variety of human tissues. The invention also provides a method for producing proteins from these polynucleotide sequences. The proteins are useful for identifying compounds that modulate their activity and production. The sequences of the invention are useful for treating diseases such as hyperproliferative disorders (e.g. cancer), immune deficiency disorders (e.g. severe combined immunodeficiency (SCID)), autoimmune disorders (e.g. multiple sclerosis), blood disorders (e.g. thrombocytopaenia), inflammatory disorders (e.g. arthritis), infectious disorders (e.g. hamanatory disorders (e.g. arthritis), infectious disorders (e.g. hamanatory disease), liver fibrosis, coagulation disorders (e.g. haemophila), and tumours. The polynucleotide sequences of the invention are also useful in gene therapy. ABK35610-ABK36232 represent the CONA sequences of the invention that encode for Gaps ö immune deficiencies and disorders such as autoimmune disorders DB 6; Length 1928; novel cDNA Sequence 1928 BP; 468 A; 535 C; 511 G; 413 T; 0 U; 1 Other; Indels present invention relates to the isolation of 7; 35 1 ATCCAGATTCTTGGCGGTAGAGAGCTGCTTGGTCA 59.5%; Score 23.8; I 80.0%; Pred. No. 13; tive 0; Mismatches Claim 1; Page 369-370; 393pp; English novel human secreted proteins Local Similarity 80.0 Query Match Matches Š

176 ATCCAAATTCTTGGCCTAGGGATGTGCTTTTTCA 142 Human cDNA sequence SEQ ID NO:14860. AAH16123 standard; cDNA; 2343 BP (first entry) 26-JUN-2001 AAH16123; AAH16123/c RESULT 7

g

ö

Gaps

ö

Human; primer; detection; diagnosis; antisense therapy; gene therapy; ss. 99JP-00248036. 99JP-00300253. 2000JP-00118776. 28-JUL-2000; 2000EP-00116126 EP1074617-A2. Homo sapiens 11-JAN-2000; 29-JUL-1999; 27-AUG-1999; 02-MAY-2000; 07-FEB-2001, 

Yamamoto J; nikawa T, Hayashi K, Saito K, Y₁ Wakamatsu A, Nagai K, Otsuki T; sogai T, Nishikawa T, Sugiyama T, Wakamatsı WPI; 2001-318749/34. Isogai T, Ishii S,

09-JUN-2000; 2000JP-00241899

(HELI-) HELIX RES INST.

Claim 8; SEQ ID NO 14860; 2537pp + Sequence Listing; English.

Primer sets for synthesizing polynucleotides, particularly the 5602 fulllength cDNAs defined in the specification, and for the detection and/or diagnosis of the abnormality of the proteins encoded by the full-length

The present invention describes primer sets for synthesising 5602 full-

```
length cDNAs defined in the specification. Where a primer set comprises:

(a) an oligo-dT primer and an oligonucleotide complementary to the complementary strand of a polynucleotide which comprises one of the S602 nucleotide sequences defined in the specification, where the oligonucleotide comprises at least 15 nucleotides; or (b) a combination of an oligonucleotide comprising a sequence complementary to the complementary strand of a polynucleotide which comprises a 3'-end sequence and an oligonucleotide which comprises a 3'-end sequence, where the oligonucleotide which comprises a 3'-end sequence, where the oligonucleotide which comprises a 3'-end sequence, where the oligonucleotide comprises a 3'-end sequence, where the comprises at least 15 nucleotides and the combination of the 5'-end sequence is selected from those defined in the specification. The primer sets can be used in antisense therapy and in gene therapy. The primer sets can be used in antisense therapy and in gene therapy. The primer sets can be used in antisense therapy and in gene therapy. The primer sets can be used in antisense therapy and in cancellation and/or diagnosis of the abnormality of the proteins endode by the full-length cDNAs. The primers are also useful for the cDNAs easily without any specialised methods. AAH03166 to AAH13628 and AAH13623 to AAH13622 represent the numan amino acid sequences; and AAH13622 to AAH13632 represent coligonucleotides, all of which are used in the exemplification of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        present invention
```

ö DB 4; Length 2343; Sequence 2343 BP; 569 A; 643 C; 625 G; 506 T; 0 U; 0 Other; 7; Indels 1 ATCCAGATTCTTGGCGGTAGAGAGCTGCTTGGTCA 35 ; Score 23.8; DB ; Pred. No. 14; 0; Mismatches Query Match
Best Local Similarity 80.0%;
Matches 28; Conservative

ö

Gaps

591 ATCCAAATTCTTGGCGCTAGGGATGTGCTTTTTCA 557 g

8

AAH14062 standard; cDNA; 2390 BP AAH14062; 

(first entry) 26-JUN-2001 Human cDNA sequence SEQ ID NO:11199.

Human; primer; detection; diagnosis; antisense therapy; gene therapy; ss.

Homo sapiens

BP1074617-A2

07-FEB-2001.

28-JUL-2000; 2000BP-00116126

99JP-00248036. 99JP-00300253. 2000JP-00118776. 27-AUG-1999; 11-JAN-2000; 29-JUL-1999;

02-MAY-2000; 2000JP-00183767 09-JUN-2000; 2000JP-00241899

(HELI-) HELIX RES INST.

Isogai T, Nishikawa T, Hayashi K, Saito K, Yamamoto J; Sugiyama T, Wakamatsu A, Nagai K, Otsuki T; Ota T, IB IBhii S,

WPI; 2001-318749/34.

Primer sets for synthesizing polynucleotides, particularly the 5602 full-length cDNAs defined in the specification, and for the detection and/or diagnosis of the abnormality of the proteins encoded by the full-length CDNAB.

Claim 8; SEQ ID NO 11199; 2537pp + Sequence Listing; English

```
ö
                                                                                                                                                                                                                                                                                                                                                                                     DRASP; replication; repair; treatment; prophylaxis; diagnosis; screening; anemia; spliepsy; hypothyroidism; cancer; autoimmune disease; AIDS; acquired immune deficiency syndrome; atherosclerosis; autoimmune thyroiditis; bronchitis; allergy; asthma; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /product= "DNA replication and repair associated protein"
                                                                                                                                                                                                                                       Gapa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New proteins useful for diagnosing, treating or preventing disorders
                                                                                                                                                                                                                                                                                                                                                                     Sequence encoding DNA replication and repair associated protein.
                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Baughn MR, Reddy R, Guegler KJ, Yue H;
                                                                                                                                                                                                                  Score 23.8; DB 4; Length 2390;
Pred. No. 14;
0; Mismatches 7; Indels 0.
                                                                                                                                                                                                    Sequence 2390 BP; 580 A; 656 C; 639 G; 515 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                        649 Arccaaarrcrrccccraccarcrccrrrrca 615
                                                                                                                                                                                                                                                       35
                                                                                                                                                                                                                                                        1 ATCCAGATTCTTGGCGGTAGAGAGCTGCTTGGTCA
                                                                                                                                                                                                                                                                                                                                                                                                                                               Location/Qualifiers
                                                                                                                                                                                                                                                                                                                  AAZ93150 standard; DNA; 2650 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             99WO-US017800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              98US-0155245P.
                                                                                                                                                                                                                      59.5%;
                                                                                                                                                                                                                                                                                                                                                    19-JUN-2000 (first entry)
                                                                                                                                                                                                                   Query Match 59.5
Best Local Similarity 80.0
Matches 28; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                          .2317
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (INCY-) INCYTE PHARM INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /*tag=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Corley NC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2000-205711/18
                                                                                                                                                                                     present invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  P-PSDB; AAY82742
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WO200008156-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             06-AUG-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               07-AUG-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      27-AUG-1998;
                                                                                                                                                                                                                                                                                                                                    AAZ93150;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        rang YT,
                                                                                                                                                                                                                                                                                                           AAZ93150/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Key
                                                                                                                                                                                                                                                                                                  RESULT 9
                                                                                                                                                                                                                                                                                                                                     $$$$$$$$$$$$$$$$$$$$$$$$$$$$
                                                                                                                                                                                                                                                        ઠ
                                                                                                                                                                                                                                                                        셤
```

```
DNA replication and repair associated proteins (DRASP) and their antigonists are useful for treating or preventing a disease associated with increased expression or activity of DRASP. These disorders include development disorders e.g anemia, epilepsy, hypothyroidism, proliferative disorders including cancer; autoimmune/inflammatory disorders including AIDS, atherosclerosis, autoimmune thyroiditis; bronchitis; allergies and asthma. The DRASP s and the polymucleotides encoding them are also useful for diagnosis of the above mentioned disorders. Catalytic or immunogenic fragments of the DRASP or its oligopeptides can be useful for screening libraries of compounds in a variety of drug screening techniques
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         antificumatic; antiproliferative; cytostatic; cardiant; vasotropic; cerebroprotective; nootropic; neuroprotective; antibacterial; virucide; fungicide; ophthalmological; gene therapy; autoimmune disease; infection; hyperproliferative disorder; cardiovascular disorder; angiogenesis; cerebrovascular disorder; nervous system disorder; ocular disorder; wound healing; skin aging; food additive; preservative; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Isolated nucleic acid molecule encoding a human secreted protein is used in preventing, treating or ameliorating a medical condition.
associated with expression of DNA replication- and repair- associated proteins.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human; secreted protein; diagnosis; immunosuppressive; antiarthritic;
                                                                                                                                                                                                                                                                                                                                       Length 2650;
                                                                                                                                                                                                                                                                                                  Sequence 2650 BP; 667 A; 697 C; 710 G; 576 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                          7:
                                                                                                                                                                                                                                                                                                                                 Score 23.8; DB 3;
Pred. No. 14;
                                                                                                                                                                                                                                                                                                                                                                                                                                            883 Arccaaarrcrrccccracccarcrccrrrrca 849
                                                                                                                                                                                                                                                                                                                                                                                                             1 ATCCAGATTCTTGGCGGTAGAGAGCTGCTTGGTCA 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human secreted protein gene 47 SEQ ID NO:57.
                                                                                                                                                                                                                                                                                                                                                                        0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 1; Page 461-462; 540pp; English.
                                                                  Claim 9; Page 68-69; 70pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Komatsoulis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAC93410 standard; cDNA; 2770 BP
                                                                                                                                                                                                                                                                                                                                       59.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               06-APR-2000; 2000WO-US009069
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                09-APR-1999; 99US-0128702P.
20-JAN-2000; 2000US-0177049P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (HUMA-) HUMAN GENOME SCI INC (ROSE/) ROSEN C A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          26-FEB-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity 80.0
Matches 28; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Rosen CA, Ruben SM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2000-619225/59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            P-PSDB; AAB51666
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WO200061620-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            19-0CT-2000.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAC93410;
                                                                                                                                                                                                                                                                                                                                     Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAC93410,
                ሯ
                                                                                                                                                                                                                                                                                                                                                                                                                                            셤
```

The polynucleotide sequences given in AAC93364 to AAC93412 encode the human secreted proteins given in AAB51620 to AAB51668. AAB51669 to AAB51722 represent human secreted polypeptide sequences and proteins homologous to them, which are given in the exemplification of the present

ö

Gaps

```
Invention, numan secreted processes activities based on the tissues and cells the genes are expressed in. Examples of activities include: antiarthritic; immunosuppressive; antirheumatic; antiproliferative; cytostatic; cardiant; vasotropic; cerebroprotective; nootropic; cerebroprotective; antibacterial; virucide; fungicide; and controprotective; antibacterial; virucide; fungicide; and be used to pervent, treat or ameliorate a medical condition in e.g. humans, mice, rabbits, goats, horses, cats, dogs, chickens or sheep. They are also used in diagnosing a pathological condition or susceptibility to a pathological condition. Disorders which are diagnosed or treated include autoimmume diseases, hyperproliferative disorders, cardiovascular disorders, angiogenesis, nervous system clisorders, infections caused by bacteria, viruses and fungi and ocular disorders. Infections caused by bacteria, viruses and fungi and ocular clisorders in polypoptides can also be used to aid wound healing and ceptimelial cell proliferation, to prevent skin aging due to sumburn, to maintain organs before transplantation, for supporting cell culture of polypoptides can also be used as alion be used to preservative to increase or decrease storage capabilities. AAC93355 to AAC93363 and AABS1619 represent sequences which are used in the exemplification of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Primer sets for synthesizing polynucleotides, particularly the 5602 full-length cDNAs defined in the specification, and for the detection and/or diagnosis of the abnormality of the proteins encoded by the full-length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human; primer; detection; diagnosis; antisense therapy; gene therapy; ss.
invention. Human secreted proteins have activities based on the tissues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Yamamoto J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 3; Length 2770;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 8; SEQ ID NO 17110; 2537pp + Sequence Listing; English
                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 2770 BP; 703 A; 721 C; 746 G; 598 T; 0 U; 2 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ë
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Saito K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1001 ATCCAAATTCTTGGCGCTAGGGATGTGCTTTTTCA 967
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Isogai T, Nishikawa T, Hayashi K, S
, Sugiyama T, Wakamatsu A, Nagai K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 ATCCAGATTCTTGGCGGTAGAGAGCTGCTTGGTCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; Score 23.8; DB
; Pred. No. 14;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human cDNA sequence SEQ ID NO:17110.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAH17602/c
ID AAH17602 standard; cDNA; 2892
                                                                                                                                                                                                                                                                                                                                                                                                                                                               59.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   28-JUL-2000; 2000EP-00116126.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         27-AUG-1999; 99JP-00300253.
11-JAN-2000; 2000JP-00118776.
02-MAX-2000; 2000JP-00183767.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           99JP-00248036
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   09-JUN-2000; 2000JP-00241899
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity 80.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (HELI-) HELIX RES INST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2001-318749/34.
                                                                                                                                                                                                                                                                                                                                                                                        present invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EP1074617-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           29-JUL-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      26-JUN-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 07-FEB-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAH17602;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ishii S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CDNAB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches
 ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           셤
```

```
The present invention describes primer sets for synthesising 5602 full-
length cDNAs defined in the specification. Where a primer set comprises:

(a) an oligo-dr primer and an oligonucleotide complementary to the complementary strand of a polynucleotide which comprises one of the 5602 nucleotide sequences defined in the specification, where the oligonucleotide comprises at least 15 nucleotides; or (b) a combination of an oligonucleotide comprising a sequence complementary to the complementary strand of a polynucleotide which comprises a 5'-end sequence and an oligonucleotide comprising a sequence complementary to a polynucleotide comprises a 3'-end sequence of an oligonucleotide comprises a 3'-end sequence of the 5'-end sequence and an oligonucleotide comprises a 3'-end sequence of polynucleotide comprises at least 15 nucleotides and the combination of the 5'-end sequence 3'-end sequence in selected from those defined in the specification. The primer sets can be used in antisense therapy and in gene therapy. The primers are useful for synthesising polynucleotides, specification and/or diagnosis of the abnormality of the proteins encoded by the full-length cDNAs. The primers are also useful for the full-length cDNAs. The primers allow obtaining of the full-length cDNAs assily without any specialised methods. AAH13612 for AAH13613 to AAH13613 represent human amino acid sequences; and AAH13623 to AAH13612 represent complementary and in the exemplification of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               present invention
```

Sequence 2892 BP; 721 A; 756 C; 785 G; 630 T; 0 U; 0 Other;

Gaps ö Score 23.8; DB 4; Length 2892; Pred. No. 14; 0; Mismatches 7; Indels 0 1144 ATCCAAATTCTTGGCGCTAGGGATGTGCTTTTTCA 1110 1 ATCCAGATICTTGGCGGTAGAGAGCTGCTTGGTCA 35 59.5%; Best Local Similarity 80.0%; Matches 28; Conservative Query Match 셤 8

ö

ABQ54736 standard; cDNA; 3134 BP ABQ54736; RESULT 12 ABQ54736, 

22-AUG-2002 (first entry)

Human ovarian antigen HOCPY47 cDNA, SEQ ID NO:616.

Human; ovarian antigen; ovary; ovarian; breast; cancer; tumour; ovarian cancer; breast cancer; tumour; reproductive system disorder; infertility; pregnancy disorder; anovulation; polycystic ovary syndrome; PCOS; ovarian cyst; dysmenorrhoea; endocrine disorder; infection; inflammatory condition; immune disorder; blood disorder; cardiovascular disorder; respiratory disorder; neurological disorder; gentrointestinal disorder; urinary system disorder; drug screening; gene therapy; chromosome mapping; forensic analysis; antibody preparation; cytostatic; immunomodulatory; neuroprotective; antibody preparation; cytostatic; immunomodulatory; neuroprotective; antibodiammatory; gynaecological; reproductive; gene; ss.

ношо варіепв

WO200200677-A1

03-JAN-2002.

07-JUN-2001; 2001WO-US018569

07-JUN-2000; 2000US-0209467P.

(HUMA-) HUMAN GENOME

Rosen CA; Birse CE,

WPI; 2002-147878/19.

P-PSDB; ABP41659

Isolated nucleic acid molecules encoding novel ovarian polypeptides,

```
The invention relates to 2175 novel human ovarian antigens (ABP41054-ABP43228) and to cDNAs encoding them (ABQ54131-ABQ56305), and also encompasses polypeptides 90% identical and polymucleotides 95% identical to the sequences of the invention. The invention additionally relates to recombinant vectors and host cells comprising human ovarian antigens or polymucleotides, antibodies against human ovarian antigens, and the use of ovarian polymucleotides and polypeptides in diagnosing, treating, prognosing or preventing various ovary and/or breast cancer, and disorders. Such conditions include ovarian cancer and breast cancer, and metastatic tumours of ovarian or breast origin, reproductive system disorders (e.g., infertility, disorders of pregnancy, anovulation, polycystic ovary syndrome, ovarian cysts, and dysmenorrhoes), endocrine disorders, infertility, disorders (e.g., mastitis, oophoritis and cysts, and dysmenorrhoes), inflammatory conditions (e.g., mastitis, oophoritis and conditions (e.g., mastitis, oophoritis and conditions (e.g., mastitis, oophoritis and using should alsorders (e.g., anaemia), cardiovascular disorders and urinary system disorders. Ovarian antigen polypeptides and conditions (e.g., anaemia), cardiovascular disorders and urinary system disorders. Ovarian antigen polypeptides and conditions (e.g., anaemia), cardiovascular disorders and urinary system tisorders. Ovarian antigen polypeptides may also be used in screening for compounds which modulate ovarian antigen expression or activity. The polymucleotides may be used as food additives or to prepare antibodies therefor in disease diagnosis, drug targeting and phenotyping. The present colypeptides may be used as food additives or to prepare antibodies useful in disease diagnosis, drug targeting and phenotyping. The present colypeptides may be used as food additives or to prepare antibodies conversed to the printed specification, but was obtained in electronic format directly from WIPO at ftp.whpo.int/published_pot_preserver.
useful in the prevention, treatment and diagnosis of cancer (e.g. ov cancer), immune disorders, cardiovascular disorders and neurological
                                                                                                                         Claim 1; SEQ ID NO 616; 2922pp; English
                                                                     diseases.
```

Sequence 3134 BP; 789 A; 801 C; 855 G; 678 T; 0 U; 11 Other;

Gaps . 0 DB 6; Length 3134; Indels 7; Query Match
59.5%; Score 23.8; D
Best Local Similarity 80.0%; Pred. No. 15;
Matches 28; Conservative 0; Mismatches

ö

1330 Arcchartrcrrccccracccarcrccrrrrca 1296 1 ATCCAGATTCTTGGCGGTAGAGAGCTGCTTGGTCA 35 셤 ઠે

AAH16661 standard; cDNA; 6701 AAH16661/c RESULT 13 

26-JUN-2001 (first entry)

AAH16661;

Human cDNA sequence SEQ ID NO:15799.

Human; primer; detection; diagnosis; antisense therapy; gene therapy; ss.

Homo sapiens.

EP1074617-A2

07-FEB-2001

28-JUL-2000; 2000EP-00116126

29-JUL-1999; 27-AUG-1999;

27-AUG-1999; 99JP-00300253. 11-JAN-2000; 2000JP-00118776. 02-MAY-2000; 2000JP-00183767. 09-JUN-2000; 2000JP-00241899.

Φ

```
Primer sets for synthesizing polynucleotides, particularly the 5602 full-length cDNAs defined in the specification, and for the detection and/or diagnosis of the abnormality of the proteins encoded by the full-length
                                                                                                                                                                                                                                                                             represent human amino acid sequences; and AAH13629 to AAH13632 represent oligonucleotides, all of which are used in the exemplification of the
                                                                                                 Claim 8; SEQ ID NO 15799; 2537pp + Sequence Listing; English.
                ogai T, Nishikawa T, Hayashi K, Saito K, Yi
Sugiyama T, Wakamatsu A, Nagai K, Otsuki T;
(HELI-) HELIX RES INST.
                                        WPI; 2001-318749/34.
                 Isogai T,
                                                                                                                                                                                                                                                                                              present invention
                        Ishii S,
                                                                                   CDNAB.
```

Gaps Sequence 6701 BP; 1676 A; 1812 C; 1722 G; 1491 T; 0 U; 0 Other; ö ch 59.5%; Score 23.8; DB 4; Length 6701; 1 Similarity 80.0%; Pred. No. 17; 28; Conservative 0; Mismatches 7; Indels 0; Best Local Similarity Query Match Matches

ö

4953 ATCCAAATTCTTGGCGCTAGGGATGTGCTTTTTCA 4919 1 ATCCAGATTCTTGGCGGTAGAGAGCTGCTTGGTCA 35 셤

ACA56981 standard; cDNA; 7228 BP ACA56981; 

10-JUN-2003 (first entry)

Human adipocyte Selected Interacting domain, SID, cDNA #68.

Human; 88; gene; prey; adipocyte; SID; selected interacting domain; anorectic; antidiabetic; protein-protein interaction; diabetes; yeast 2-hybrid assay; metabolic disorder; obesity.

Homo sapiens.

31-OCT-2002.

WO200286122-A2

14-MAR-2002; 2002WO-EP003768

14-MAR-2001; 2001US-0275734P

(HYBR-) HYBRIGENICS

Legrain P, Daviet L;

Yamamoto J;

WPI; 2003-103412/09. P-PSDB; ABU70437 complex between two interacting proteins in adipocyte cells, useful identifying selected interacting domains that modulate protein gractions, or for preventing or treating metabolic disorders such as New complex between obesity or diabetes interactions,

Claim 7; Page 134-138; 382pp; English.

The invention relates to a complex between two interacting proteins in adipocyte cells, given in the specification. The proteins are identified by selecting a bait protein from a known adipocyte marker and then performing a peak 2-hybrid selection to isolate prey proteins are cooled by commence of an adipocyte cDNA library. The proteins are designated SID (RTM) (selected interacting domains) proteins. Also included are a polymeptide encoding a polymeptide in the adipocyte cells, a complex, selecting a modulating compound in adipocyte cells, a SID (RTM) polymeptide comprising any of the 738 amino acid sequences given in the specification (including its fragment or variant), cells, a SID (RTM) polymelectide comprising any of the 738 nucleotide sequences given in the specification (including its fragment or variant), comprising the SID (RTM) polymuloctide, a recombinant host cell comprising the vector, a protein chip comprising the polymeptides and a record comprising all or part of the data, listed in the specification. The complex, polymeptides, polymelectides and compounds are useful for the complex, polymeptides, polymelectides and compounds are useful for man encoded the second comprising or treating or treating or treating or treating metabolic disorders such as observed the second comprising or treating or treating or preventing or treating or treating or preventing or treating or protein complex, when the specification comprised the second comprised The polynucleotides are useful as probes or primers. The complex is particularly useful for identifying selected interacting domains (SI (RTM)) for screening drugs that modulate the protein interaction, the exhibiting the therapeutic effect. The present sequence encodes a SI (prey) protein of the invention

Sequence 7228 BP; 1822 A; 1955 C; 1903 G; 1548 T; 0 U; 0 Other;

Gaps ö DB 8; Length 7228; Indels 7; Query Match
59.5%; Score 23.8; D
Best Local Similarity 80.0%; Pred. No. 17;
Matches 28; Conservative 0; Mismatches

ö

5794 Arccaaarrcrrccccraccaraccarcrrcrrca 5760 35 1 ATCCAGATTCTTGGCGGTAGAGAGCTGCTTGGTCA 셤

AAS44988 standard; cDNA; 7747 BP AAS44988/c RESULT 15 

(first entry) 18-DEC-2001

AAS44988;

cDNA encoding novel human secretory protein, Seg ID No 69.

Human; secreted protein; arthritis; Crohn's disease; sepsis; shock; ischaemia-reperfusion injury; haematopoiesis; cancer; neuropathy; transgenic animal; Alzheimer's disease; Parkinson's disease; burn; amyotrophic lateral sclerosis; platelet disorder; thrombocytopenia; ulcer; osteoporosis; bone degenerative disorder; periodontal disease; gut protection; lung; liver fibrosis; immune deficiency; infection; severe combined immunodeficiency; SCID; autoimmune disorder; allergy; multiple sclerosis; rheumatoid arthritis; diabetes mellitus; asthma; fertility; analgesic; pain; antigen; se.

WO200166689-A2

13-SEP-2001

```
The invention relates to novel isolated human secreted polypeptides (I) and polynucleotides (II). (I) and (II) are useful for treating inflammatory conditions such as arthritis, nephritis, crohif a disease, ischaemia-reperfusion injury, shock, sepsis, immune responses, and is involved in increasing haematopoiesis, stem cell survival, bone growth and remodaling. (I), (II) and modulators of (II) are useful for prophylaxis or treatment of one or more cancers. (II) is also useful for creating transgenic animals useful for studying the in vivo activities of the polypeptides. (I) induces the proliferation of neutral cells and regeneration of nerve and brain tissue and is useful for the treatment of central and compared in addition, (I) is involved in chemotactic or chemokinetic sclerosis. In addition, (I) is involved in chemotactic or chemokinetic cortismes. The polyment and for regeneration of haematopoiesis and is useful for treating myeloid or lissue growth, and in tissue repair, healing of burns, incisions, ulcers, for treating osteoporosis, osteoarthritis, bone degenerative disorders, cor periodontal disease. Purthermore, (I) is also useful for gut protection or regeneration and treatment of lung or liver invarious fimmine deficiencies and its unique immine and cortismes and cortismes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           reperfusion or regimenation and treatment or 1 mag of 1104 1101019; protection of regimenation and treatment of 1 mag of 1104 intercions and combined immunodeficiency (SCID), bacterial or fungal infections, autoimmune disorders e.g. multiple scienciss, in remarking a matching severe combined immunodeficiency (SCID), bacterial or remarking a tribritis, diabetes mellitus, myasthenia gravis, allergic reactions and conditions, such as asthma or other respiratory problems. In addition, (1) affects biorhythms or circadian cycles of thythms, fertility, metabolism, catabolism, anabolism, storage or elimination of dietary fat, lipid, protein, carbohydrate, vitamins, minerals, provides activity and can act as an anigen in a vaccine composition to raise an immune response. AAS44929-AAS45295 represent novel human secreted protein
                                                                                                                                                                                                                                                                                                                                                                      Tang YT, Liu C, Asundi V, Xu C, Wehrman T, Ren F, Ma Y, Zhou P;
Zhao QA, Yang Y, Drmanac RT, Zhang J, Chen R, Xue AJ, Wang J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Novel polypeptides and nucleic acids obtained from cDNA libraries prepared from various human tissues, for diagnosis and treatment of cancer, neurological, inflammatory, and autoimmune disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 1; SEQ ID NO 69; 107pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              coding sequences of the invention
                                                                                                                  ; 2000US-00574454.
; 2000US-00596193.
; 2000US-00616847.
; 2000US-00665363.
                             05-MAR-2001; 2001WO-US004942
                                                                                                                                                                                                                                             20-OCT-2000; 2000US-00693267
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2001-589934/66.
                                                                                                                                                                                                                                                                                                           (HYSE-) HYSEQ INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     P-PSDB; AAU28088
                                                                                                                                                                               14-JUL-2000;
                                                                                                                                                     17-JUN-2000;
                                                                                                                        19-MAY-2000;
```

Sequence 7747 BP; 1948 A; 2083 C; 2034 G; 1682 T; 0 U; 0 Other;

Gaps ö DB 5; Length 7747; 7; Indels Query Match 59.5%; Score 23.8; D Best Local Similarity 80.0%; Pred. No. 18; Matches 28; Conservative 0; Mismatches

ö

ઠે

Search completed: April 18, 2006, 19:13:01 Job time : 222 secs

This Page Blank (uspto)

601473137 601277738 K-EST0108 60210821 UI-E-E01-602414648 603178537 CR992502 602737128

Title: Perfect score:

Run on:

Scoring table: Sequence:

Searched:

**Database** 

```
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia; Butheria; Laurasiatheria, Cetartiodactyla, Ruminantia; Pecora, Bovinae; Bos.

1 (Dases 1 to 513)

2 Smith,T.P.L., Grosse,W.M., Freking,B.A., Roberts,A.J., Stone,R.T., Casas,E., Wray,J.B., White,J., Cho,J., Rahrenkrug,S.C., Dennett,G.L., Heaton,M.P., Laegreid,W.W., Rohrer,G.A., Chisko-McKown,C.G., Pertes,G., Holt,I., Karamycheva,S., Liang,F., Quackenbush,J. and Reele,J.W.

Sequence evaluation of four pooled-tissue normalized bovine cDNA libraries and construction of a gene index for cattle Genome Res. 11 (4), 626-630 (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Tel: 402 762 4366

Pax: 402 762 4396

Brail: smith@email.marc.usda.gov

Single pass sequencing. Bases called and alt trimmed with phred

vo.980904.e. Vector identified by cross_match with the -minscore 18

pand -minmatch 12 options.
                                               BE619266
BB38410
BM83752
BG749832
BG749832
BE905313
BM724099
BG388908
BG388908
CT000492
CT000492
CT000492
CT000492
BG764111
CT000492
BG764111
BF3131328
BF3131328
BF3131328
BF3131328
BF3131328
BF3131328
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BE682696 535 bp mRNA linear 180928 MARC 4BOV Bos taurus CDNA 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Contact: Smith TPL
USDA, ARS, US Meat Animal Research Center
PO Box 166, Clay Center, NE 68933-0166, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                        ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1. .535
/organism="Bos taurus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FORWARD: AGGAAACAGCTATGACCAT
BACKWARD: GTTTTCCCAGTCACGACG
Plate: 75 row: C column: 23
Seq primer: ATTTAGGTGACACTATAG.
                                                                                                                                                                                                                         CT000492
CR980220
BP23482
AU132166
BG753212
B1913289
BF338327
BG536386
AU124415
                                                                                                                                                                        B1916606
CR992502
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BE682696
BE682696.1 GI:10068819
Bos taurus (cow)
Bos taurus
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOUNCE
ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 1
BE682696/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  JOURNAL
PUBMED
COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REFERENCE
AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TITLE
BE682696 180928 MA
BG391395 602417472
AA957723 U.R.E1-G
BF420664 UI-R-BL2-
BF557216 UI-R-E1-G
CK843614 UI-R-BL2-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BF557216 UI-R-E1-G
CK643614 UI-R-BJ2-
AA143624 zo65gO7.r
BG318970 PM4-CT054
BQ318970 PM4-CT054
BQ318970 PM4-CT054
BA479493 25564 MAR
BF767919 CM1-CN006
AA153119 zo59e04.r
CD673609 f802e10.y
BR486052 171917 BA
DN601950 HBSC3 74
AM579072 RCO-CT038
BM712229 UI-R-DW1-
BP264713 BP264713
CB15078 KST0206
BP364411 BP344471
                                                                                                                   April 18, 2006, 19:13:18; Search time 1706.5 Seconds (without alignments) 1096.679 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Description
                                                                                                                                                                                                                                                                                                                                                    82156650
              GenCore version 5.1.7
Copyright (c) 1993 - 2006 Biocceleration Ltd
                                                                                                                                                                                                                           atccagattcttggcggtagagagctgcttggtcagactt 40
                                                                                                                                                                                                                                                                                                                41078325 seqs, 23393541228 residues
                                                                                                                                                                                                                                                                                                                                                 Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                                                                                       Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                      OM nucleic - nucleic search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BF557216
CK843614
AA13624
AA13624
BG952796
BG318970
AA159119
AA159119
CD673609
BR45052
DN601950
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BG391395
AA957723
BF420664
                                                                                                                                                                                                                                                            IDENTITY NUC Gapop 10.0 , Gapext 0.1
                                                                                                                                                                                                                                                                                                                                                                                     Minimum DB seq length: 0
Maximum DB seq length: 200000000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               9b_est1:*
9b_est2:*
9b_htc::-
9b_est4:*
9b_est4:*
9b_est7:*
9b_est7:*
9b_gss2:*
                                                                                                                                                                                          SEQ4 - THEN - SEQ3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query
Match Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             5000

5000

5000

5000

5000

5000

5000

5000

5000

5000

5000

5000

5000

5000

5000

5000

5000

5000

5000

5000

5000

5000

5000

5000

5000

5000

5000

5000

5000

5000

5000

5000

5000

5000

5000

5000

5000

5000

5000

5000

5000

5000

5000

5000

5000

5000

5000

5000

5000

5000

5000

5000

5000

5000

5000

5000

5000

5000

5000

5000

5000

5000

5000

5000

5000

5000

5000

5000

5000

5000

5000

5000

5000

5000

5000

5000

5000

5000

5000

5000

5000

5000

5000

5000

5000

5000

5000

5000

5000

5000

5000

5000

5000

5000

5000

5000

5000

5000

5000

5000

5000

5000

5000

5000

5000

5000

5000

5000

5000

5000

5000

5000

5000

5000

5000

5000

5000

5000

5000

5000

5000

5000

5000

5000

5000

5000

5000

5000

5000

5000

5000

5000

5000

5000

5000

5000

5000

5000

5000

5000

5000

5000

5000

5000

5000

5000

5000

5000

5000

5000

5000

5000

5000

5000

5000

5000

5000

5000

5000

5000

5000

5000

5000

5000

5000

5000

5000

5000

5000

5000

5000

5000

5000

5000

5000

5000

5000

5000

5000

5000

5000

5000

5000

5000

5000

5000

5000

5000

5000

5000

5000

5000

5000

5000

5000

5000

5000

5000

5000

5000

5000

5000

5000

5000

5000

5000

5000

5000

5000

5000

5000

5000

5000

5000

5000

5000

5000

5000

5000

5000

5000

5000

5000

5000

5000

5000

5000

5000

5000

5000

5000

5000

5000

5000

5000

5000

5000

5000

5000

5000

5000

5000

5000

5000

5000

5000

5000

5000

5000

5000

5000

5000

5000

5000

5000

5000

5000

5000

5000

5000

5000

5000

5000

5000

5000

5000

5000

5000

5000

5000

5000

5000

5000

5000

5000

5000

5000

5000

5000

5000

5000

5000

5000

5000

5000

5000

5000

5000

5000

5000

5000

5000

5000

5000

5000

5000

5000

5000

5000

5000

5000

5000

5000

5000

5000

5000

5000

5000

5000

5000

5000

5000

5000

5000

5000

5000

5000

5000

5000

5000

5000

5000

5000

5000

5000

5000

5000

5000

5000

5000

5000

5000

5000

5000

5000

5000

5000

5000

5000

5000

5000
```

EST 25-APR-2001

/molltype="mRNA" /db_xref="taxon:9913" /tfswue_type="pooled" /lab_host="#01108" /clone_lib="MARC 4BOV" /note="Vector: pCMV SPORT6; Site_1: Not1; Site_2: Sal1;

AW579072 BM712229 BP264713

220 221 220 221 231 251

0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0

Result Š. CB150078 BP196040 BP344471

AU132166 602731604 603180045 602035559 602564779 AU124415

CT000492 CR980220 BP223482

ORIGIN

```
Rattus norvegicus

Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Bukaryota, Butheria, Buarchontoglires, Glires, Rodentia,
Sciurognathi, Muroidea, Muridae, Murinae, Rattus.

1 (bases 1 to 456)

Bonaldo,M.F., Lennon, G. and Soares, M.B.

Normalization and subtraction: two approaches to facilitate gene
                                                                                                                                                                                                            On May 7, 1998 this sequence version replaced gi:3121418
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 24.6; DB 1; Length 456; Pred. No. 64; 0; Mismatches 9; Indels
                                                                                                                                                                                                                                       Contact: Soares, MB
Coordinated Laboratory for Computational Genomics
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        369 Arccrearrerreccearacacaacacerrecceacacr 331
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 ATCCAGATTCTTGGCGGTAGAGAGCTGCTTGGTCAGACT
                                                                                                                                                                                  Genome Res. 6 (9), 791-806 (1996)
                    Rattus norvegicus (Norway rat)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        iocation/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 61.5%;
Best Local Similarity 76.9%;
Matches 30; Conservative (
                                                                                                                                                                discovery
                                                                                                                                                                                                    8889548
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             source
                                   ORGANISM
                                                                                                                                                                              JOURNAL
PUBMED
COMMENT
                                                                                                                           AUTHORS
TITLE
                                                                                                           EFERENCE
 KEYWORDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ሯ
                                                                                                             ö
                                                                                                                                                                                                                                                                           BG391395 17472F1 NIH_MGC_92 Homo sapiens cDNA clone IMAGE:4537192 5',
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EST 04-JUL-1999
                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.

1 (Danses 1 to 748)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbe.r@mail.nih.gov
Tissue Procurement: ATCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /tissue_type="embryonal carcinoma, cell line"
/lab.host="DH10B (phage-resistant)"
/clone_lib="NIH MGC_blage"
/note="Organ: testis; Vector: pCMV-SPORT6; Site_1: Not1;
Site_2: Sall; Cloned unidirectionally; oligo-dT primed.
Average insert size_2: S. Rb. Library enriched for
full-length clones and constructed by Life Technologies.
Note: this is a NIH_MGC Library."
Library made from pooled tissue from day 20 and day 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.B. Consortium (LIML)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.B. Consortium/LLNL at:
http://image.llnl.gov. oclumn: 17
                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             456 bp mRNA linear BST 04-JU
UI-R-EI-gc-a-12-0-UI.sl UI-R-EI Rattus norvegicus cDNA clone
AA957723
AA957723.1 GI:4277613
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 62.0%; Score 24.8; DB 2; Length 748; Best Local Similarity 80.6%; Pred. No. 57; Matches 29; Conservative 0; Mismatches 7; Indels
                                                                       Length 535;
                                                                                                           Indels
                                                                                                           9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             585 Arccaarrcrrescerasesarerecrrrreas 550
                                                                      Score 25.4; DB 2;
Pred. No. 31;
0; Mismatches 6;
                                                                                                                                                                                294 Arccadarrcrredecegrededargrecrrea 260
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 ATCCAGATTCTTGGCGGTAGAGAGCTGCTTGGTCAG 36
                                                                                                                                               1 ATCCAGATTCTTGGCGGTAGAGAGCTGCTTGGTCA 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Plate: LLAM10461 row: o column: 17
High quality sequence stop: 734.
Location/Qualiflers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGB:4537192"
                                                                                                                                                                                                                                                                                                                                                 BG391395.1 GI:13284843
                                                                    Query Match 63.5%;
Best Local Similarity 82.9%;
Matches 29; Conservative
                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens (human)
                    embryos."
                                                                                                                                                                                                                                                                                                              mRNA sequence.
BG391395
                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 3
AA957723/c
LOCUS
```

source

ORIGIN

ઠે 셤

PEATURES

VERSION KEYWORDS SOURCE ORGANISM

ACCESSION

TITLE JOURNAL COMMENT

REFERENCE AUTHORS

RESULT 2 BG391395/c DEFINITION

ઠે

ô

Gapa

ö

DEFINITION

ACCESSION

VERSION

EST 12-DEC-2000

VERSION KEYWORDS SOURCE ORGANISM

ACCESSION

AUTHORS TITLE

JOURNAL PUBMED

COMMENT

REFERENCE

BF420664/c LOCUS

```
/organism="katcus norvegicus"
//wol type="mRNA"
// strain="Sprague-Dawley"
// strain="Sprague-Dawley"
// db xef="thexon:10116"
// lab host="Dulu"
// lab in the diluged (Life Technologies) "
// lab in the diluged (Life Technologies) to generate the diluged (Life Technologies) to generate the UI-R-EI library in the form of blooble-stranded circles and electroporated into DH10B hacteria (Life Technologies) to generate the UI-R-EI library. This procedure has been previously described (Bonaldo, Lennon and Soares, Genome Research 6: 791-806, 1996) "
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Email: bento-soares@ulowa.edu

CDNA Library Preparation: M.B. Soares Lab Clone distribution:

CDNA Library Preparation: M.B. Soares Lab Clone distribution:

Clones will be available through Research Genetics (www.resgen.com)

This clone is also available through the I.M.A.G.B. Consortium at

LLNL (infc@image.llnl.gov). IMAGE ID= 1772375 The following

repertitive elements were found in this cDNA sequence: 253-472,

>MERAILB#LTR/MER4-group

Seq primer: MI3 Forward.
                                                                                                                                                                                                                                                                                                    Eukaryota; Mecazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                          1 (bases 1 to 502)
Bonaldo,M.F., Lennon,G. and Soares,M.B.
Normalization and subtraction: two approaches to facilitate gene
BF557216
UI-R-E1-gc-a-12-0-UI.rl UI-R-E1 Rattus norvegicus cDNA clone
UI-R-E1-gc-a-12-0-UI 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  University of Iowa
375 Newton Road , 4156 MEBRP, Iowa City, IA 52242, USA
Tel: 319 335 8250
Fax: 319 335 9565
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 2; Length 502;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Contact: Soares, MB
Coordinated Laboratory for Computational Genomics
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        422 ATCCTGATTCTTGCCGATAGACAACAGCTTGCCCACACT 460
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 ATCCAGATTCTTGGCGGTAGAGAGCTGCTTGGTCAGACT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /organism="Rattus norvegicus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61.5%; Book. 76.9%; Pred. No. 65,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Genome Res. 6 (9), 791-806 (1996)
                                                                                                                                                                                                                                    Rattus norvegicus (Norway rat)
Rattus norvegicus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Location/Qualifiers
                                                                                                                      BF557216.1 GI:11666946
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 76.9'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           8889548
                                           DEFINITION
                                                                                                                                                                                                                                                                        ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AUTHORS
TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        JOURNAL
PUBMED
COMMENT
                                                                                                                      ACCESSION
                                                                                                                                                     VERSION
KEYWORDS
SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                              REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /Brandle Dyservation control of the Apparation of the Indian and the Apparation of t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The sequence contained an oligo-dT track that was present in the oligonucleotide that was used to prime the synthesis of first strand cDNA and therefore this may represent a bonsfide poly A tail. The sequence tag present in the cDNA between the NoII site and the oligo-dT track served to identify it as a clone from the normalized arrium at 16.5 dpc library cDNA library Preparation: M.B. Soares Lab Clone distribution: clones will be available through Research Genetics (www.resgen.com) The following repetitive elements were found in this cDNA sequence: 141-278, SKSINEL#SINE/B4 (BS 302-483, >MER31B#LTR/MER4-group
                                                                              BF420664
UI-R-BJ2-bpy-f-09-0-UI.sl UI-R-BJ2 Rattus norvegicus cDNA clone
UI-R-BJ2-bpy-f-09-0-UI 3', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Butheria; Buarchontoglires; Glires; Rodentia; Sciurognathi; Muroidea; Muridae; Rattus.

1 (Dases 1 to 484)
Bonaldo,M.F., Lennon,G. and Soares,M.B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            375 Newton Road , 4156 MEBRP, Iowa City, IA 52242, USA Tel: 319 335 8265 Pax: 319 355 9565 Email: bento-soares@uiowa.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61.5%; Score 24.6; DB 2; Length 484; 76.9%; Pred. No. 64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Contact: Soares, MB
Coordinated Laboratory for Computational Genomics
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           9; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     370 ATCCTGATTCTTGCCGATAGACAACAGCTTGCCCACACT 332
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 ATCCAGATTCTTGGCGGTAGAGGCTGCTTGGTCAGACT 39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Lennon and Soares, Genome Resurt TAG TISSUE-atrium at 16.5 dpc TAG LIB-UI-R-BU2 TAG LIB-UI-R-BU2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /organism="Rattus norvegicus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /mol_type="mRNA"
/strain="Sprague-Dawley"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Genome Res. 6 (9), 791-806 (1996)
                                                                                                                                                                                                                                                                                                               Rattus norvegicus (Norway rat)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Location/Qualifiers
                                                                                                                                                                                                                            BF420664.1 GI:11408653
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             University of Iowa
375 Newton Road , 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local Similarity 76.9 tes 30; Conservative
                                                                                                                                                                                                                                                                                                                                                       norvegicus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           discovery
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     POLYA=Yes
                                                                                                                                                                                                 BF420664
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              8889548
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
```

source

FEATURES

ö

Gape

ö

Indels

6

Matches

8

ORIGIN

RESULT 5 BPS57216

RESULT 6 CK843614/c

LOCUS

KEYWORDS SOURCE ORGANISM

JOURNAL PUBMED COMMENT

AUTHORS TITLE RFERENCE

ACCESSION VERSION

```
NS9506 349 bp mRNA linear EST 28-JAN-1997 yv57e07.rl Soares fetal liver spleen INFLS Homo sapiens cDNA clone IMAGE:246852 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Hominidae; Homo.

1 (bases 1 to 349)

Hillier,L., Lennon,G., Becker,M., Bonaldo,M.F., Chiapelli,B.,

Hillstock, Lennon,G., Budque,T., Favello,A., Gish,W.,

Chissoe,S., Dietrich,N., Kucaba,T., Lacy,M., Le,M., Le,N.,

Hawkins,M., Hultman,M., Kucaba,T., Lacy,M., Le,M., Le,N.,

Mardis,R., Moore,B., Morris,M., Parsons,J., Prange,C., Rifkin,L.,

Rohlfing,T., Schellenberg,K., Soares,M.B., Tan,F., Thierry-Meg,J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini,
2065g07.rl Stratagene pancreas (#937208) Homo sapiens cDNA clone IMAGE:591804 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                       Hominidae, Homo.

1 (bases 1 to 308)

Hillier,L., Allen,M., Bowles,L., Dubuque,T., Geisel,G., Jost,S.,

Hillier,L., Allen,M., Bowles,L., Dubuque,T., Geisel,G., Jost,S.,

Krizman,D., Kucaba,T., Lacy,M., Le,N., Lennon,G., Marra,M.,

Martin,J., Moore,B., Schellenberg,K., Steptoe,M., Tan,F.,

Theising,B., White,Y., Wylie,T., Waterston,R. and Wilson,R.

Unpublished (1997)

Contact: Wilson RK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Fel: 314 286 1810
Fax: 314 286 1810
Fax: 314 286 1810
Fax: 31 286 1810
Fax: 32 20ne is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information. Insert Length: 1982 Std Error: 0.00
Seq primer: -28M13 rev2 from Amersham
High quality sequence stop: 235.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           59.5%; Score 23.8; DB 1; Length 308; 80.0%; Pred. No. 1.3e+02; ive 0; Mismatches 7; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 ATCCAGATTCTTGGCGGTAGAGAGCTGCTTGGTCA 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 53 Arccaaarrcrrccccraccaarcrccrrrrca 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /mol_type="mRNA"
/db_xref="GDB:4623190"
/db_xref="taxon:9606"
                                                                                                         AA143624.1 GI:1713056
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          N59506
N59506.1 GI:1203396
                                                                                                                                                                                Homo sapiens (human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens (human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      28; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        . .308
                                                                                                                                                                                                                         Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EST.
                                                                   ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            VERSION
KEYWORDS
SOURCE
ORGANISM
   DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TITLE
JOURNAL
COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ACCESSION
                                                                                                                                                                                                                                                                                                                                                                    REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                         AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NS9506/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ଚ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /d_one=vul-R-Bi2-bi2.
/dlone=vul-R-Bi2-bi2.
/lab_host==vul-R-Bi2-bi2.
/lab_host==vul-R-Bi2-bi2.
/dlone=lib="vul-R-Bi2"
/dlone=lib="vul-R-Bi2"
/olone=lib=vul-R-Bi2.
/note="Vector: pi7:3D-Pac (Pharmacia) with a modified
polylinker; Site 1: Not 1; Site 2: Eco RI; The UI-R-Bi2
library is a subtracted library derived from the following
tissues: heart, atrium at 15 dpc, ventricle at 16:5 dpc,
atrium at 16:5 dpc, ventricle at 13 dpc, ventricle at 15
dpc, AV canal at 15 dpc. For a detailed description of
the library from which this clone was derived, please
visit our web site at ratest.eng.ulowa.edu. The
subtraction has been previously described in (Bonaldo,
Lennon and Soares, Genome Research 6:791-806, 1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    University of lowa 375 Newton Road, 4156 MEBRF, lowa City, IA 52242, USA 7E1: 319 335 B250
Te1: 319 335 B250
Fax: 319 350 B250
Fax: 319 B250
Fax: 310 B250
F
                                                                   CK843614 1inear EST 05-MAR-2004 UI-R-BJ2-bpy-f-09-0-UI.810 UI-R-BJ2 Rattus norvegicus cDNA clone UI-R-BJ2-bpy-f-09-0-UI 3', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ó
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EST 08-NOV-1997
                                                                                                                                                                                                                                                                                                                           Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Bammalla; Butheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Muridae; Rattus.
(bases 1 to 643)
Bonaldo,M.F., Lennon,G. and Soares,M.B.
Normalization and subtraction: two approaches to facilitate gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61.5%; Score 24.6; DB 7; Length 643; 76.9%; Pred. No. 67; tive 0; Mismatches 9; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Contact: Soares, MB
Coordinated Laboratory for Computational Genomics
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    370 Arccrearrerreccearacacaacaccreeccacacr 332
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 ATCCAGATICTIGGCGGTAGAGAGCTGCTTGGTCAGACT 39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /organism="Rattus norvegicus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TAG TISSUE-atrium at 16.5 dpc
TAG LIB=UI-R-BJ2
TAG SEQ=GATTC"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /mol_type="mRNA"
/strain="Sprague-Dawley"
/db xref="taxon:10116"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Genome Res. 6 (9), 791-806 (1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        308 bp
                                                                                                                                                                                                                                                                                         Rattus norvegicus (Norway rat)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         .ocation/Qualifiers
                                                                                                                                                                                CK843614
CK843614.1 GI:45200552
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity 76.9
Matches 30; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           . .643
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          discovery
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AA143624
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             8889548
```

source

FEATURES

ö

Gaps

ö

Query Match

ઠ 셤

ORIGIN

RESULT 7 AA143624/c LOCUS

```
Homo sapiens (human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Tel: +55-11-2704922
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Brazil
                                      Brazil
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
                                                                                                                                                                                                                                          source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BQ318970/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Loc
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ACCESSION
VERSION
KEYWORDS
SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           JOURNAL
PUBMED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RBFERENCE
                                                                                                                                                                                                                       FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            용
                                                                                                                                                                                                                                                                                                                                                                                                                                     Hominidae; Homo.

1 (bases 1 to 355)
Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,
Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F.,
Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H.,
Brunstein,A., deoliveira,P.S., Bucher,P., Jongeneel,C.V.,
O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
Simpson,A.J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EST 12-JUN-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Buarchontoglires, Primates, Catarrhini,
revaskis,E., Underwood,K., Wohldmann,P., Waterston,R., Wilson,R.
                                Generation and analysis of 280,000 human expressed sequence tags
Genome Res. 6 (9), 807-828 (1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Shotgun sequencing of the human transcriptome with ORF expressed
                                                                                                                                                                             Email: est@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Insert Length: 1771 Std Brror: 0.00
Seq primer: T7
High quality sequence stop: 297.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         355 bp mRNA linear EST 12.
PM4-CT0543-200101-001-c06_1 CT0543 Homo sapiens cDNA, mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                       Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               sequence tags
Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
1037800
Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 23.8; DB 8; Length 349;
Pred. No. 1.3e+02;
0; Mismatches 7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                169 Arcchartrcrrecceraeceargicarrrica 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 ATCCAGATTCTTGGCGGTAGAGAGCTGCTTGGTCA 35
                                                                                                                                                                                                                                                                                                                              /organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                               /mol_type="mRNA"
/db_xref="GDB:3796098"
/db_xref="taxon:9606"
/clone="IMAGE:246852"
                                                                                                                                                                                                                                                                                              Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GI:14370967
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       59.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                          /sex="male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens (human)
                                                                                     Contact: Wilson RK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 59.5
Best Local Similarity 80.0
Matches 28; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BG952796.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 sequence.
                                                                                                                                                                                                                                                                                                                   Bource
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 9
BG952796/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ORGANISM
                                  TITLE
JOURNAL
PUBMED
COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PUBMED
COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    VERSION
KEYWORDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                JOURNAL
                                                                                                                                                                                                                                                                                              PRATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               δ
```

```
Fax: +55-11-2707001

Email: asimpson@ludwig.org.br
This asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=PM4&t2=PM4-CT0543-
200101.001-c06_1&tal=22001-01-20&t4=1)
Seq primer: puc 18 forward
High quality sequence stops: 355.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Hominidae; Homo.

1 (bases 1 to 355)
Diss Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R., Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F., Goldman,G.H., Carvalho,A.F., Matsukuma,A., Bala,G.S., Simpson,D.H., Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EST 17-MAY-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Fax: +55-11-2707001

Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=PM4&t2=PM4-CT0543-290900-001-c06_l&t3=2000-09-29&t4=1)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Anotes Organ: colon, Vector: pucle, Site 1: Smal, Site 2: Smal, A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the DUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Buarchontoglires, Primates, Catarrhini,
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Shotgun sequencing of the human transcriptome with ORF expressed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BQ318970 355 bp mRNA linear EST 17<sup>,</sup>
PM4-CT0543-290900-001-c06_l CT0543 Homo sapiens cDNA, mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bequence tags
Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
10737800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 355;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indele
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 23.8; DB 2;
Pred. No. 1.3e+02;
0; Mismatches 7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         314 ArccaaArrcrrecceracearcrecrrrrea 280
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 ATCCAGATTCTTGGCGGTAGAGAGCTGCTTGGTCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /organism="Homo sapiens"
/mol_type="mRNA"
/mol_type="mRNA"
/db_xref="taxon:9606"
/dev_stage="Adult"
/clone_lib="CT0543"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             stringency conditions.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BQ318970
BQ318970.1 GI:20924739
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Match 59.5%;
Local Similarity 80.0%;
es 28; Conservative
```

ö

seq4-then-seq3.rst

```
1 (bases 1 to 367)
Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R.,
Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F.,
Goldman, G.H., Carvalho, A.F., Matsukuma, A., Baia, G.S., Simpson, D.H.,
Brunstein, A., deoliveira, P.S., Bucher, P., Jongeneel, C.V.,
O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /dev_stage="Adult"
/clone lib="CN0061"
/clone lib="CN0061"
/note="Organ: colon normal; Vector: puc18; Site_1: Smal;
Site_2: Smal; A minI-library was made by cloning products
derived from ORESTES PCR (U.S. Letters Patent application
No. 196,776 - Ludwig Institute for Cancer Research)
profiles into the puC 18 vector. Reverse transcription of
tissue mRNA and cDNA amplification were performed under
                                                                                                                                                                                                                                                                                                                                  EST 12-JAN-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Fax: +55-11-2707001
Bmail: asimpson@ludwig.org.br
Fax: 1-55-11-2707001
Bmail: sainpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=CM1&t2=CM1-CN0061-201200-673-g909&t5=2000-12-20&t4=1)
Seq primer: puc 18 forward
High quality sequence start: 3
High quality sequence stop: 364.
                                                                                                                                                                                                                                                                                                                                                        CM1-CN0061-201200-673-g09 CN0061 Homo sapiens cDNA, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Shotgun sequencing of the human transcriptome with ORF expressed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                       Gaps
                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
                                                                         Length 358;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 367;
                                                                      Score 23.8; DB 1; Length 3 Pred. No. 1.3e+02; 0; Mismatches 7; Indels
                                                                                                                                                                                                                                                                                                                                  linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    59.5%; Score 23.8; DB 2;
80.0%; Pred. No. 1.3e+02;
ive 0; Mismatches 7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 35
                                                                                                                                                                 35
                                                                                                                                                                                                               44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             125 Arccaaarrcrrccccracccaarcrccrrrrca 91
                                                                                                                                                                                                                                                                                                                                  mRNA
                                                                                                                                                                                                               78 Arccagarrcrrcccccccccarcrccrrca
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 ATCCAGATTCTTGGCGGTAGAGAGCTGCTTGGTCA
                                                                                                                                                                   1 ATCCAGATTCTTGGCGGTAGAGAGCTGCTTGGTCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  low stringency conditions."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /mol_type="mRNA"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                367
                                                                                                                                                                                                                                                                                                                                                                                                         BF767919.1 GI:12115819
                                                                      59.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens (human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       rel: +55-11-2704922
                                                               Ouery Match
Best Local Similarity 80.0°
Matches 28; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1. .367
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               sequence tags
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity
nes 28; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                10737800
                                                                                                                                                                                                                                                                                                                                BF767919
                                                                                                                                                                                                                                                                                                                                                                                   BF767919
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bource
                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOURCE
                                                                                                                                                                                                                                                                                                            BF767919/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Loca
Matches
                                                                                                                                                                                                                                                                                                                                                           DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                 ACCESSION
VERSION
KEYWORDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PUBMED
COMMENT
                                                                                                                                                                                                                                                                                      RESULT 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PEATURES
                             ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ORIGIN
                                                                                                                                                                                                                                                                                                                                     LOCUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             g
                                                                                                                                                                                                               셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Email: smith@email.marc.usda.gov
Single pass sequencing. Bases called and trimmed with phred
vo.980904.e. Vector identified by cross_match with the -minscore 20
and -minmatch 12 options.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                /mol_type="mRNA"
/db xref="taxon:9906"
/db xref="taxon:9906"
/db_gatage="Adult"
/clone_lib="Cr0543"
/note="Organ: colon; Vector: puc18; Site_l: Smal; Site_2:
Smal; A mini-library was made by cloning products derived
from ORBSTES PCR (U.S. Letters Patent application No.
196,716 - Ludwig Institute for Cancer Research) profiles
into the pUC 18 vector. Reverse transcription of tissue
mRNA and cDNA amplification were performed under low
stringency conditions."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EST 25-APR-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi, Mammalia, Butherla, Laurasiatheria, Cetartiodactyla, Ruminantia, Bordae, Bovinae, Bos.

1 (Dases 1 to 358)
Smith, T.P.L., Grosse, M.M., Freking, B.A., Roberts, A.J., Stone, R.T., Casas, E., Wary, J.E., White, J., Cho, J., Fahrenkrug, S.C., Bennett, G.L., Heaton, M.P., Laegreid, W.W., Rohrer, G.A., Chitko-McKown, C.G., Pertea, G., Holt, I., Karamycheva, S., Liang, F., Guackenbush, J. and Keele, J.W.
Sequence evaluation of four pooled-tissue normalized bovine cDNA libraries and construction of a gene index for cattle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /clone lib="MARC 4BOV"
/note="Vector: pCMV SPORT6; Site 1: Not1; Site 2: Sal1;
Library made from pooled tissue from day 20 and day 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                             Length 355;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AW479483 358 bp mRNA linear 25564 MARC 4BOV Bos taurus cDNA 5', mRNA sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Contact: Smith TPL
USDA, ARS, US Meat Animal Research Center
PO Box 166, Clay Center, NE 68933-0166, USA
TEL: 402 762 4366
Fax: 402 762 4390
                                                                                                                                                                                                                                                                                                                                                                                                              Score 23.8; DB 3; I
Pred. No. 1.3e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 314 ATCCAAATTCTTGGCGCTAGGGATGTGCTTTTTCA 280
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 ATCCAGATTCTTGGCGGTAGAGAGCTGCTTGGTCA 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Mismatches
                                                                                               /organism="Homo sapiens"
Seg primer: puc 18 forward
High quality seguence stop: 355.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1. .358
/organism="Bos taurus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FORWARD: AGGAAACAGCTATGACCAT
BACKWARD: GTTTCCCAGTCACGACG
Plate: 12 row: K column: 12
Seg primer: ATTTAGGTGACACTATAG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /mol_type="mRNA"
/db_xref="taxon:9913"
/tissue_type="pooled"
/lab_host="DH108"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AW479483.1 GI:7049589
                                                                                                                                                                                                                                                                                                                                                                                                                               59.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                28; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bos taurus (cow)
                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bos taurus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AW479483
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 11282978
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DEFINITION
ACCESSION
VERSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bource
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AW479483/c
LOCUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PUBMED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     KEYWORDS
                                                FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMMENT
                                                                                                                                                                                                                                                                                                                                                                                   ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOURCE
```

유

```
/clone_libe_Human Lens cDNA (Normalized): fs"
/clone_libe_Human Lens cDNA (Normalized): fs"
Inter="Gorgan: Bye; Vector: pCWVSPORT6; A human lens
library (by) was normalized by self-subtraction. One
portion of double stranded plasmid DNA representing the
library was linearized by Norl. This Norl digested library
was used as a template for biotinylated RNA synthesis
using SP6 RNA polymarses. Another portion of the double
stranded plasmid library was converted to single-stranded
circles in vitro using Gene II and Exonuclease III (Life
Technologies). Single-stranded DNA (1 mg) was hybridized
(Cut 500) with 41 mg of Bio-RNA and vector blocking
oligonuclectides. The Hybridized Bio-RNA/ss-circles were
removed by streptavidin;phenol extraction. EST analysis
was performed on the library at the NIH Intramural
Wistow,G., Bernstein,S.L., Wyatt,M.K., Behal,A., Touchman,J.W.,
Bouffard,G., Smith,D. and Peterson,K.
Expressed sequence tag analysis of adult human lens for the NEIBank
Project: over 2000 non-redundant transcripts, novel genes and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EST 27-MAR-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Analysis of bovine mammary gland EST and functional annotation of the Bos taurus gene index Mamm. Genome 13 (7), 373-379 (2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Butheria; Laurasiatheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae; Bovinae; Bos.
1 (basea 1 to 471)
Sonstegard, T., Capuco, A.V., White, J., Van Tassell, C.P., Connor, B.B., Cho, J., Sultana, R., Shade, L., Wray, J.E., Wells, K.D. and Quackenbush, J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     6; Length 443;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BE485052 471 bp mRNA linear 111917 BARC 5BOV BOB taurus CDNA 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Contact: Sonstegard TS
USDA, ARS, Beltsville Agricultural Research Center
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                          Section on Molecular Structure and Function
National Eye Institute
6/31, NIH, Bethesda, MD 20892-2740, USA
TTE1: 301 402 3452
Fax: 301 496 0078
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 59.5%; Score 23.8; DB 6; Best Local Similarity 80.0%; Pred. No. 1.3e+02; Matches 28; Conservative 0; Mismatches 7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      164 ArccaaArrcrrececraecearerecrrrrrea 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 ATCCAGATTCTTGGCGGTAGAGAGCTGCTTGGTCA 35
                                                                                                                                                                                                                                                                                     Email: graeme@helix.nih.gov
Plate: 02 row: e column: 10
Seg primer: M13RP1 reverse primer (ABI).
                                                                                                                                                                                                                                                                                                                                                                                                   /organism="Homo sapiens"
/mol type="mxNA"
/db xref="taxon:9606"
/clone="f802e10"
/fissue type="tens"
/dev stage="Adult"
/lab_nost="EMDH108"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequencing Center (NISC)."
                                                                                 splice variants
Mol. Vis. 8 (4), 171-184 (2002)
12107413
                                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BE485052.1 GI:9604585
                                                                                                                                                       Contact: Wistow G
                                                                                                                                                                                                                                                                                                                                                                                       1. .443
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bos taurus (cow)
Bos taurus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BE485052
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BST.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                     source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Loca
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BE485052/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LOCUS
                                                                                                         JOURNAL
PUBMED
COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PUBMED
COMMENT
AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    JOURNAL
                                                                                                                                                                                                                                                                                                                                                           PEATURES
                                            TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DRIGIN
                                                                                      EST 09-MAR-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             443 bp mRNA linear EST 24-JUN-2003
f802e10.yl Human Lens cDNA (Normalized): f8 Homo sapiens cDNA clone
raceseto 5., mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                              Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 0.356)

1 Hillier,L., Allen,M., Bowles,L., Dubuque,T., Geisel,G., Jost,S., Krizman,D., Kucaba,T., Lacy,M., Le,N., Lennon,G., Marra,M., Martin,J., Moore,B., Schellenberg,K., Steptoe,M., Tan,P., Theising,B., White,Y., Wylie,T., Waterston,R. and Wilson,R. WashU-NCI human EST Project
Unpublished (1997)

Contact: Wilson RK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi;
Mammalia, Butheria, Buarchontoglires, Primates, Catarrhini;
                                                          436 bp mRNA linear EST 09-MAR-15
2059e04.rl Stratagene pancreas (#937208) Homo sapiens CDNA clone
1NAGE:591198 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Email: est@watson.wustl.edu
This clone is available royalty-free through LLNL ; contact the
IMAGE Consortium (inf@dimage.llnl.gov) for further information.
IMAGE Chimer: 28M13 rev2 from Amersham
High quality sequence stop: 232.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 436;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 23.8; DB 1;
Pred. No. 1.3e+02;
0; Mismatches 7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       205 ATCCAAATTCTTGGCGCTAGGGATGTGCTTTTTCA 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 ATCCAGATTCTTGGCGGTAGAGAGCTGCTTGGTCA 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="GDB:4622584"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CD673609.1 GI:32175340
                                                                                                                                                                            AA159119.1 GI:1733930
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    59.5%;
                                                                                                                                                                                                                    Homo sapiens (human)
Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens (human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Hominidae; Homo.
1 (bases 1 to 443)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              28; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1. .436
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
                                     RESULT 13
AA159119/c
                                                                                 LOCUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOURCE
ORGANISM
                                                                                                                                                                                                                      SOURCE
ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 14
CD673609/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LOCUS
                                                                                                                                                                                                                                                                                                                                    REFERENCE
AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                               TITLE
JOURNAL
COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches
                                                                                                                                                     ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ACCESSION
                                                                                                                                                                          VERSION
KEYWORDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             VERSION
KEYWORDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ORIGIN
```

셤

```
Bdlg. 200 Rm 2A, Beltsville, MD 20705, USA
Tel: 301 504 8416
Fax: 301 504 8414
Fax: 301 504 8414
Email: tadsolpsi.barc.usda.gov
Single pass sequencing. Bases called and alt_trimmed with phred
v0.980904.e. Vector identified by cross_match with the -minscore 18
and -minmatch 12 options.
PCR PRIMERS
FORWAND: AGGAAACAGCTATGACCAT
BACKWAND: GTTTCCAGTACGACG
Plate: 134 row: A column: 20
Seq primer: ATTAGGTGACACTATAG.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1. 471

Organism=Bos taurus"

/mol_type="mkNa"

/db_xrefe="taxon:9913"

/db_xref="barbon:9913"

/lab_bost="barbons"

/lab_bost="barbons"

/lab_bost="barbons"

/lab_bost="barbons"

/lab_bost="parbons"

/lab_bost="barbons"

/lab_bost="barbons
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 59.5%; Score 23.8; DB 2; Length 471; Best Local Similarity 80.0%; Pred. No. 1.3e+02; Matches 28; Conservative 0; Mismatches 7; Indels C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 ATCCAGATTCTTGGCGGTAGAGGCTGCTTGGTCA 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ORIGIN
```

133 ATCCAGATTCTTGGCGCTGGGGATGTGCTTCTTCA 99

g ò

Search completed: April 18, 2006, 20:10:22 Job time : 1710.5 secs

Sequence 4, Appli Sequence 3, Appli Sequence 1764, Appli Sequence 1764, App Sequence 110, Ap Sequence 4705, Ap Sequence 4705, Ap Sequence 4705, Ap Sequence 4231, Ap Sequence 1201, Ap Sequence 1201, Ap Sequence 96389, A Sequence 96389, A Sequence 96389, A Sequence 96654, A Sequence 96655, A Sequence 96655, A

```
US-09-938-642-4
US-09-938-540-3
US-09-938-540-3
US-09-938-540-1
US-09-938-540-1
US-09-938-540-1
US-09-533-559-4705
US-09-533-559-4705
US-09-620-312D-825
US-09-949-016-96389
US-09-949-016-96389
US-09-949-016-96653
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ATCCAGATTCTTGGCGGTAGAGAGCTGCTTGG
                                                                                                                                                                                                                                                    ALIGNMENTS
 20
20
20
20
20
1600
1950
1893
2330
2330
2330
2330
601
601
601
601
601
601
  υυ
                                                                                       000 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Š
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 104, Appli
Sequence 983, App
Sequence 983, App
Sequence 17215, A
Sequence 1081, Ap
Sequence 11805, A
Sequence 11805, A
Sequence 12962, A
Sequence 12962, A
Sequence 12962, A
Sequence 2849, A
Sequence 2646, A
Sequence 2646, A
Sequence 262, Appli
Sequence 292, Appli
                                                                        April 18, 2006, 19:28:37 ; Search time 73.5 Seconds (without alignments) 967.380 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                        Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
             GenCore version 5.1.7
Copyright (c) 1993 - 2006 Biocceleration Ltd
                                                                                                                                                                                                                     2606114
                                                                                                                                                                                                                                                                                                                             /cgn2_6/ptodata/1/ina/1_COMB.seq:*
/cgn2_6/ptodata/1/ina/5_COMB.seq:*
/cgn2_6/ptodata/1/ina/6_COMB.seq:*
/cgn2_6/ptodata/1/ina/H_COMB.seq:*
/cgn2_6/ptodata/1/ina/H_COMB.seq:*
/cgn2_6/ptodata/1/ina/H_COMB.seq:*
/cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
/cgn2_6/ptodata/1/ina/PP_COMB.seq:*
/cgn2_6/ptodata/1/ina/PP_COMB.seq:*
/cgn2_6/ptodata/1/ina/RE_COMB.seq:*
/cgn2_6/ptodata/1/ina/RE_COMB.seq:*
                                                                                                                                           1 atccagattcttggcggtagagagctgcttggtcagactt
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-09-620-312D-104

US-09-938-540-1

US-09-949-016-17215

US-09-949-016-17215

US-08-956-171E-4081

US-08-956-171E-4081

US-08-78-1-986A-4081

US-09-949-016-11862

US-09-949-016-11862

US-09-949-016-11863

US-09-949-016-11863

US-09-949-016-118649

US-09-910-181-292

US-09-910-840A-2

US-09-991-181-292

US-09-991-181-292

US-09-991-181-292

US-09-992-333-292

US-09-992-333-292

US-09-994-016-17361

US-09-994-016-17361

US-09-994-016-17361
                                                                                                                                                                                                                    Total number of hits satisfying chosen parameters:
                                                                                                                                                                                               1303057 seqs, 888780828 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SUMMARIES
                                                                                                                                                                                                                                                                         Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                        nucleic search, using sw model
                                                                                                                                                               IDENTITY NUC Gapop 10.0 , Gapext 0.1
                                                                                                                                                                                                                                                                                                                     Patents NA:*
                                                                                                                                                                                                                                          seq length: 0
seq length: 200000000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        56.5 7827 3
54.0 23193 3
54.0 23193 3
52.0 359 3
52.0 359 3
52.0 3191 3
52.0 3191 3
51.0 629 3
51.0 481152
50.5 1484 3
50.5 767677 3
50.5 767677 3
                                                                                                                      SEQ4-THEN-SEQ3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query
Match 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Title:
Perfect score:
                                                                                                                                                                 Scoring table:
                                                                                                                                                                                                                                          Minimum DB E
Maximum DB E
                                                       nucleic
                                                                                                                                            Sequence:
                                                                                                                                                                                                 Searched:
                                                                                                                                                                                                                                                                                                                      Database
                                                                             Run on:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Result
                                                         ₹
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               \circ \circ \circ \circ \circ \circ \circ \circ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   υυυ
```

Z 5	RESULT 1 US-09-620-312D-104/c
••••	Sequence 104, Application US/09620312D Patent No. 6569662
	GENERAL INFORMATION: APPLICANT: Tang, Y. Tom
••••	AFFLICANT: Abundi, vinca APPLICANT: Zhang. Jie
	_
••	Chen,
••	APPLICANT: Zhao, Qing A.
•••	
• ••	
•••	Wang,
•	
•	
_	wang,
	APPLICANT: Wang, Zniwel
	NVENTION: No. 6569
	TITLE OF INVENTION: Polypeptides
•	FILE REFERENCE: 784CIP2B
	Ħ
	CURRENT FILING DATE: 2000-07-19
	APPLICATION N
••	PRIOR FILING DATE: 2000-04-25
<u></u>	PRIOR APPLICATION NUMBER: 09/488,725
•	PRIOR FILING DATE: 2000-01-21
•	
••	SOFTWARE: pt_FL_genes Version 1.0
•	~
••	LENGTH: 7827
•	TYPE: DNA
_	ORGANISM: Homo sapiens
•	
	SOS
••	LOCATION: (121)(7497)
Ď 	US-09-620-312D-104
	59.5%; Score 23.
	Best Local Similarity 80.0%; Pred. No. 5.9; Matches 28; Conservative 0; Mismatches 7; Indels 0; Gaps 0;
ۇ 	1 ATCCAGATTCTTGGCGGTAGAGGCTGCTTGGTCA 35

```
Sequence 13444, Application US/09949016

Sequence 13444, Application US/09949016

Batent No. 681239

GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CL001307
CURRENT APPLICATION NUMBER: 60/241,755
PRIOR PELING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/231,768
PRIOR PILING DATE: 2000-10-03
PRIOR PILING DATE: 2000-10-03
PRIOR PILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012

SOFTWARE: PastSEQ for Windows Version 4.0

SEQ ID NO 13444
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT PILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR APPLICATION NUMBER: 60/231,768
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR PILING DATE: 2000-10-03
PRIOR PILING DATE: 2000-00-08
PRIOR PILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE PARESEQ for Windows Version 4.0
SEQ ID NO 17215
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 21.6; DB 3; Length 23193;
Pred. No. 57;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 21, DB 3; Length 172677;
Pred. No. 1.5e+02;
0; Mismatches 5; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                10082 rcriacacacacacacicriccriccraa 10054
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            4048 rerrrecrecadadadecrecrrecrea 4021
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TGGTCAGA 37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      9 TCTTGGCGGTAGAGAGCTGCTTGGTCAG 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 4081, Application US/08956171E
Patent No. 6533114
GENERAL INFORMATION:
APPLICANT: Charles Kunsch
G11 H. Choi
Patrick S. Dillon
                                                                                                                                                                                                                                                                                                                                                          | FEATURE:
| NAME/KEY: misc_feature
| LOCATION: (1)...(23193)
| OTHER INFORMATION: n = A,T,C or G
| US-09-949-016-17215
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 85.7%;
Matches 24; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 52.5%;
Best Local Similarity 82.8%;
Matches 24; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           9 TCTTGGCGGTAGAGAGCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-09-949-016-13444/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-08-956-171E-4081/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; ORGANISM: Human
US-09-949-016-13444
                                                                                                                                                                                                                                                                                                                    TYPE: DNA
ORGANISM: Human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ठ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ઠ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 3
US-09-248-796A-983/c
i Sequence 983, Application US/09248796A
j Patent No. 6747137
j GENERAL INFORMATION:
j APPLICANT: Keith Weinstock et al
j TITLE OF INVENTION: NUCLEIC ACID AND THERAPEUTICS
j TITLE OF INVENTION: NUMBER: US/09/248,796A
j TITLE OF INVENTION: NUMBER: US/09/248,796A
j CURRENT APPLICATION NUMBER: US/09/248,796A
j CURRENT PILING DATE: 1999-02-12
j FRIOR PILING DATE: 1998-02-13
j PRIOR PILING DATE: 1998-02-13
j PRIOR FILING DATE: 1998-08-13
j PRIOR FILING DATE: 1998-08-13
j NUMBER OF SEQ ID NOS: 28208
j SEQ ID NO 983
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                  Sequence 1, Application US/09938540
Patent No. 6838267
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Degussa AG
APPLICANT: DEGUSS BT
CURRENT APPLICATION NUMBER: US/09/938,540
CURRENT APPLICATION NUMBER: US/09/938,540
CURRENT FILING DATE: 2001-08-27
NUMBER OF SEQ ID NOS: 4
SOFTWARE: PATENTIN VET: 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 1600;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 663;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-09-949-016-17215/c
; Sequence 17215, Application US/09949016
; Patent No. 681233
; Patent NFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 9; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   978 Arccacarricrrescestrascerecerarragacasa 942
                             6063 Arccaaarrcrrececraeegargrecrrrrea 6029
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 ATCCAGATTCTTGGCGGTAGAGAGCTGCTTGGTCAGA 37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         140 Arccagrrrcrrgaaggraagararrcrrggr 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 22.6; DB
Pred. No. 13;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 21.8; DB; Pred. No. 24; 0; Mismatches
      TYPE: DNA ORGANISM: Corynebacterium glutamicum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   56.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 54.5%;
Best Local Similarity 78.8%;
Matches 26; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               OTHER INFORMATION: ccpAl-Gen
US-09-938-540-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 75.7
Matches 28; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: DNA ORGANISM: Candida albicans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME/KEY: CDS
LOCATION: (225)..(1388)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-09-248-796A-983
                                                                                             RESULT 2
US-09-938-540-1/c
                                                                                                                                                                                                                                                                                                                                                             SEQ ID NO 1
LENGTH: 1600
                                                                                                                                                                                                                                                                                                                                                                                                                                                        FEATURE:
                               셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       g
```

ö

```
ZIP: 20850
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    263 GATTATTGGAGGTAGAGCACTGTTTGGTACGA 232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        109 ATTGTGGGGGGAAGAGCTGCTGGCTAGAC 78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        6 GATTCTTGGCGGTAGAGAGCTGCTTGGTCAGA 37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             7 ATTCTTGGCGGTAGAGAGCTGCTTGGTCAGAC 38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 52.0%; Score 20.8; I Best Local Similarity 78.1%; Pred. No. 55; Matches 25; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE: Human Genome Sciences, Inc. STREET: 9410 Key West Avenue CITY: Rockville STATE: Maryland COUNTRY: USA
FILING DATE:
CLASSIFTCATION: 435
FRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
FILING DATE:
FILING DATE:
ATORNEY/AGENT INFORMATION:
NAME: Benson, Bob.
REGISTRATION NUMBER: PB248PP
TELEFORMINICATION INFORMATION:
TELEFORMINICATION INFORMATION:
TELEFORMINICATION 1090-8514
INFORMATION FOR SEQ ID NO: 4081:
SEQUENCE CHARACTERISTICS:
LENGTH: 359 base pairs
TYPE: nucleic acid
STRANDENNES:
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; TYPE: DNA
; ORGANISM: Drosophila melanogaster
US-09-270-767-13105
                                                                                                                                                                                                                                                                                                                                                                                                        linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-09-270-767-13105/c
                                                                                                                                                                                                                                                                                                                                                                                                        ; TOPOLOGY: 1
US-08-781-986A-4081
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-08-961-527-182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ઠે
                                              Michael R. Pannon
Michael R. Pannon
Michael R. Pannon
NUMBER OF SEQUENCES: 5256
CORRESPONDENCES: 5256
CORRESPONDENCE ADDRESSE:
ADDRESSEE: Human Genome Sciences, Inc.
STREET: 9410 Key West Avenue
CITY: Rockville
CITY: Maryland
COUNTRY: USA
ZIP: 20850
ZIP: 20850
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-08-781-986A-4081/c

Sequence 4081, Application US/08781986A

Sequence 4081, Application US/08781986A

GENERAL INFORMATION:
APPLICANT: Charles Kunsch
TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences
NUMBER OF SEQUENCES: 5255

CORRESPONDENCE ADDRESS:
ADDRESSER: Human Genome Sciences, Inc.
STREET: 9410 Key West Avenue
CITY: Rockville
STRATE: Maryland
STATE: Maryland
COUNTRY: USA
                                                                                                                                                                                                                                                                                                COMPUTER KEALALLE FORM:

WEDDIUM TYPE: Breath MEDGE WEIGH, 1.4MD storage COMPUTER: HP Vectra 486/33
OPERATING SYSTEM: MSDOS version 6.2
SOFTWARE ASCII Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/956,171E
FILING DATE: 20-Oct-1997
CLASSIFTCATION NUMBER: 60/009,861
APPLICATION NUMBER: 60/009,861
APPLICATION NUMBER: 60/009,861
APPLICATION NUMBER: 08/781,986
APPLICATION NUMBER: 08/781,986
APPLICATION NUMBER: 08/781,986
ATORNEY/AGENT INFORMATION:
NAME: MARK J. HYMMAN
REGISTRATION NUMBER: 46,789
REFERENCE/DOCKET NUMBER: PB248P1
TELEBHONE: (240) 314-1224
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 359;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               IndelB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ZIP: 20850
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
COMPUTER: HP Vectra 486/33
OPERATING SYSTEM: MSDOS version 6.2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         263 GATTATTGGAGGTAGAGCACTGTTTGGTACGA 232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GCTTGGTCAGA 37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             52.0%; Score 20.8; C 78.1%; Pred. No. 55; tive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY: linear ; SEQUENCE DESCRIPTION: SEQ ID NO: 4081: US-08-956-171E-4081
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/781,986A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (240) 314-1224
301) 309-8439
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE CHARACTERISTICS:
LENGTH: 359 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEFAX: (301) 309-84:
INFORMATION FOR SEQ ID NO: 4081
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 78.17
The 25, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    g
```

```
Sequence 182, Application US/08961527
Patent No. 6420135
GENERAL INFORMATION:
APPLICANT: Charles Kunsch
TITLE OF INVENTION: Streptococcus pneumoniae Polynucleotides and Sequences
NUMBER OF SEQUENCES: 391
CORRESPONDENCE ADDRESS:
ADDRESSEE: Human Genome Sciences, Inc.
                                                  ö
                                                                                                                                                                                                                                                                               Sequence 13105, Application US/09270767

Parent No. 6703491

GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Homburger et al.
TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
FILE REPERBNCE: File Reference: 7326-094
CURRENT APPLICATION NUMBER: US/09/270,767
CURRENT PILING DATE: 1999-03-17
NUMBER OF SEQ ID NOS: 62517
SOFTWARE: ParentIn Ver. 2.0
SEQ ID NO 13105
LENGTH: 3191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gape
                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ch 52.0%; Score 20.8; DB 3; Length 3191; Il Similarity 78.1%; Pred. No. 83; 25; Conservative 0; Mismatches 7; Indels 0
DB 3; Length 359;
                                                  Indele
```

```
51.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 74.3
Matches 26, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                           ; TYPE: DNA
; ORGANISM: Human
US-09-949-016-12962
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 13
US-09-270-767-28449
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-09-477-135A-123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-501-549-016-11863/c

US-69-949-016-11863/c

Sequence 11863, Application US/09949016

Patence 11863, Application US/09949016

GENERAL INFORMATION:

APPLICANT: VENTER.

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

CURRENT PILING DATE: 2000-04-14.755

PRIOR PILING DATE: 2000-10-03

PRIOR PILING DATE: 2000-10-03

PRIOR PILING DATE: 2000-10-03

PRIOR PILING DATE: 2000-09-08

NUMBER OF SEQ ID NOS: 207012

SOFTWARE: PRESENCE OF WINDOWS Version 4.0

SEQ ID NO 11863

LINGTHN: 35803
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 35803;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 3786;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3500 AGCCAGCTTCGTGACTGGATAGACCTGCATGGATAGACAT 3539
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              28793 GATTATTGGTTGCAGAGTCCTGCTTGGTAACTCTT 28759
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 ATCCAGATICTIGGCGGTAGAGAGCTGCTTGGTCAGACTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 52.0%; Score 20.8; DB 3;
Best Local Similarity 70.0%; Pred. No. 85;
Matches 28; Conservative 0; Mismatches 12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 20.6; DB 3;
Pred. No. 1.6e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                6 GATTCTTGGCGGTAGAGCTGCTTGGTCAGACTT 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 51.5%; Score 20.6; D
Best Local Similarity 74.3%; Pred. No. 1.6e
Matches 26; Conservative 0; Mismatches
COMPUTER: HP Vectra 486/33
OPERATING SYSTEM: MEDOS version 6.2
SOCTWARE: ASCII Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/961,527
FILING DATE:
CLASSIFICATION: 424
PRIGA APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: 36,373
FILING DATE:
ATTORNEY/AGRAT INFORMATION:
NAME: Brookes, A. Anders
REGISTRATION NUMBER: 36,373
FERERENCE/DOCKET NUMBER: 98340P1
TELEPHONE: (301) 309-8504
FILEFRAM: (301) 309-8512
FILEFRAM: 3786 Dasse pairs
FERGATH: ATRE DASSE COUBLE
FERGATH: ATRE DASSE COUBLE
FERGATH: ATRE DASSE COUBLE
FERGATH: ATRE DASSE COUBLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; TOPOLOGY: linear
US-08-961-527-182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; TYPE: DNA
; ORGANISM: Human
US-09-949-016-11863
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       g
```

US-09-949-016-12962/c ; Sequence 12962, Application US/09949016 ; Patent No. 681233 ; GENERAL INFORMATION:

```
TITLE OF INVENTION: POLYMORHENE IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: POLYMORHENE IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR PELING DATE: 2000-10-20
PRIOR PILING DATE: 2000-10-03
PRIOR PILING DATE: 2000-10-03
PRIOR PILING DATE: 2000-10-03
PRIOR PILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: PSELSEQ for Windows Version 4.0
SEQ ID NO 12962
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FARCHAL INFORMATION:
APPLICANT: Nano, Francis
TITLE OF INVENTON: Mycobacterium Tuberculosis DNA Sequences Encoding;
TITLE OF INVENTION: Mycobacterium Tuberculosis DNA Sequences Encoding;
TITLE OF INVENTION: Mycobacterium Tuberculosis DNA Sequences Encoding;
TITLE REFERENCE: 52888
FILE REFERENCE: 52888
CURRENT APPLICATION NUMBER: US/09/477,135A
CURRENT PILING DATE: 1990-01-3
PRIOR APPLICATION NUMBER: US/06/10375
PRIOR PILING DATE: 1996-06-14
PRIOR PILING DATE: 1996-06-15
NUMBER OF SEQ ID NOS: 169
SSOPIN NUMBER OF SEQ ID NOS: 169
SSOPIN NOS: 169
SSOPIN NO 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
APPLICANT: Homburger et al.
TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster FILE REFERENCE: FIPE REFERENCE: 7126-094
CURRENT APPLICATION NUMBER: 03/09/270,767
CURRENT FILING DATE: 1999-03-17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 35804;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 51.0%; Score 20.4; DB 3; Length 629; Best Local Similarity 71.1%; Pred. No. 88; Matches 27; Conservative 0; Mismatches 11; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indela
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             250 CCGAATTCTTGGCGGTGTTGACCAGCCCGGTCACCTT 213
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3 CCAGATICTIGGCGGTAGAGAGCTGCTTGGTCAGACTT 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             28793 GATTATTGGTTGCAGAGTCCTGCTTGGTAACTCTT 28759
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 20.6; DB 3;
Pred. No. 1.6e+02;
0; Mismatches 9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; Sequence 28449, Application US/09270767
; Patent No. 6703491
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-09-477-135A-123/c
; Sequence 123, Application US/09477135A
; Patent No. 6572865
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: DNA ORGANISM: Mycobacterium tuberculosis
```

```
Sequence 405, Application US/09902540
; Sequence 405, Application US/09902540
; Patent No. 6833447
; GENERAL INFORMATION:
; APPLICANT: Goldman, Barry S.
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Hinkle, Waxcoccus xanthus Genome Sequences and Uses Thereof;
; TITLE OF INVENTION: Waxcoccus xanthus Genome Sequences and Uses Thereof;
; TITLE OF INVENTION: WAXCOCCUS XANTHON TO CURRENT PILING DATE: 2001-07-10
; FRICK RAPLICATION NUMBER: 60/217,883
; PRIOR PAPLICATION NUMBER: 60/217,883
; PRIOR PRILING DATE: 2000-07-10
; NUMBER OF SEQ ID NOS: 16825
; SEQ ID NO 405.
                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Homburger et al.
TITLE APPLICANT: Homburger et al.
TITLE REPERENCE: File Reference: 7326-094
CURRENT APPLICATION NUMBER: US/09/270,767
CURRENT FILING DATE: 1999-03-17
NUMBER OF SEQ ID NOS: 62517
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 12646
LENGTH: 1891
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                   ô
                                                                                                                                                                                           Score 20.4; DB 3; Length 1627;
Pred. No. 1.18+02;
0; Mismatches 6; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
51.0%; Score 20.4; DB 3; Length 1891;
Best Local Similarity 80.0%; Pred. No. 1.1e+02;
Matches 24; Conservative 0; Mismatches 6; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 20.4; DB 3; Length 2602;
Pred. No. 1.2e+02;
0; Mismatches 6; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1487 AGAGTCTTGGAGGTAGAGCACTGATTGGAC 1458
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1057 Acccararrerrercerradadacrecer 1086
                                                                                                                                                                                                                                                                                                                                                 793 ACCCATATTCTTGTCCTTAGAGAGCTGCCT 822
                                                                                                                                                                                                                                                                                                 1 ATCCAGATTCTTGGCGGTAGAGAGCTGCTT 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 ATCCAGATTCTTGGCGGTAGAGAGCTGCTT 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        5 AGATICITGGCGGTAGAGAGCTGCTTGGTC 34
                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 14
2-09-270-767-12646
; Sequence 12646, Application US/09270767
; Patent No. 6703491
                                                                                                  ; TYPE: DNA
; ORGANISM: Drosophila melanogaster
US-09-270-767-28449
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; ORGANISM: Drosophila melanogaster
US-09-270-767-12646
                                                                                                                                                                                              Query Match 51.0%;
Best Local Similarity 80.0%;
Matches 24; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 51.0%;
Best Local Similarity 80.0%;
Matches 24; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: DNA ORGANISM: Myxococcus xanthus
NUMBER OF SEQ ID NOS: 62517
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 28449
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 15
US-09-902-540-405/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-09-902-540-405
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            a
                                                                                                                                                                                                                                                                                                   ઠ
                                                                                                                                                                                                                                                                                                                                         셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ઠે
```

Search completed: April 18, 2006, 19:31:14 Job time : 76.5 secs

This Page Blank (uspto)

```
US-10-080-381B-67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ORGANISM: RAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: DNA
Sequence 1, Appli
Sequence 57, Appl
Sequence 570, App
Sequence 510, App
Sequence 69, Appl
Sequence 69, Appl
Sequence 104, Appl
Sequence 104, Appl
Sequence 104, Appl
Sequence 104, Appl
Sequence 35, Appl
Sequence 24140, Appl
Sequence 295, Appl
Sequence 671, Appl
Sequence 671, Appl
Sequence 1385, Appl
Sequence 1385, Appl
Sequence 1185, Appl
Sequence 1185, Appl
Sequence 11, Appli
Sequence 1, Appli
                                                                        April 18, 2006, 19:39:11; Search time 675.5 Seconds (without alignments) 489.674 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Description
                                                                                                                                                                                                                                                                                                                                     / cgn2_6/ptodata/1/pubpna/USO7_PUBCOMB.seq:*
/ cgn2_6/ptodata/1/pubpna/USO8_PUBCOMB.seq:*
/ cgn2_6/ptodata/1/pubpna/USO8_PUBCOMB.seq:*
/ cgn2_6/ptodata/1/pubpna/USO9B_PUBCOMB.seq:*
/ cgn2_6/ptodata/1/pubpna/USIOA_PUBCOMB.seq:*
/ cgn2_6/ptodata/1/pubpna/USIOB_PUBCOMB.seq:*
                                                                                                                                                                                                                          19587084
         GenCore version 5.1.7
Copyright (c) 1993 - 2006 Biocceleration Ltd
                                                                                                                                            1 atccagattcttggcggtagagagctgcttggtcagactt 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-10-080-381B-1
US-09-822-846-574
US-09-822-846-574
US-09-822-846-570
US-10-264-049-616
US-10-291-172-69
US-10-291-172-69
US-10-119-926-21
US-10-119-926-21
US-10-117-722-104
US-10-112-851-104
US-10-112-851-104
US-10-112-851-104
US-10-369-493-24140
US-10-501-282-995
US-10-501-282-995
US-10-501-282-995
US-10-501-282-6651
US-10-601-282-6651
US-10-495-666-1
                                                                                                                                                                                                                       Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                  9793542 segs, 4134689005 residues
                                                                                                                                                                                                                                                                                                                            Published Applications NA Main:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-09-738-626-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-10-995-540-1
US-10-895-849-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SUMMARIES
                                                                                                                                                                                                                                                                                Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                    nucleic search, using sw model
                                                                                                                                                                   IDENTITY_NUC
Gapop 10.0 , Gapext 0.1
                                                                                                                                                                                                                                               Minimum DB seq length: 0
Maximum DB seq length: 200000000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query
Match Length DB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         900
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          860
11928
31134
6
77447
77827
7827
7827
9508
1266
1266
1266
1266
11266
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1600 3
1600 8
3309400
                                                                                                                      SEQ4 - THEN - SEQ3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      56.5
56.5
56.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Title:
Perfect score:
                                                                                                                                                                   Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     222.6
222.6
222.6
22.6
22.6
                                                       •
                                                    OM nucleic
                                                                                                                                             Sequence:
                                                                                                                                                                                                   Searched:
                                                                                                                                                                                                                                                                                                                              Database
                                                                           Run on:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Result
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Š
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             000000000000000
```

```
WS-10-080-381B-1

Sequence 1, Application US/10080381B

Publication No. US20030148421A1

GENERAL INFORMATION:
APPLICANT: USROSEN, PER BO

TITLE OF INVENTION: GENE PRODUCTS THAT REGULATE GLUCOSE RESPONSE IN CELLS

FILER REFERENCE: UTS0:773US

CURRENT APPLICATION NUMBER: US/10/080,381B

CURRENT APPLICATION NUMBER: 60/291,354

PRIOR APPLICATION NUMBER: 60/291,354

PRIOR PILING DATE: 2001-03-09

PRIOR PILING DATE: 2001-03-09

PRIOR FILING DATE: 2001-02-20

NUMBER OF SEQ ID NOS: 75

SOFTWARE: PatentIN Ver. 2.1

SEQ ID NO 1

LENGTH: 1105
Sequence 1, Appli
Sequence 13347, A
Sequence 13347, A
Sequence 615, Ap
Sequence 67134, Ap
Sequence 27134, Ap
Sequence 4979, Ap
Sequence 4979, Ap
Sequence 36171, A
Sequence 6919, A
Sequence 297054,
Sequence 139189,
Sequence 139324,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ô
                                                                                                                                                                                                                                                                                                       Sequence 345, App
Sequence 9629, Ap
Sequence 45072, A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 67, Application US/10080381B
Publication No. US20030148421A1
GENERAL INFORMATION:
APPLICANT: NEWGARD, CHRISTIPHER B.
APPLICANT: JENSEN, PER BO
TITLE OF INVENTION: GENE PRODUCTS THAT REGULATE GLUCOSE RESPONSE IN CELLS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 1105;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           742 ATCCTGATTCTTGCCGATAGACAACAGCTTGCCCACACT 780
          US-09-864-761-2916
US-09-864-761-2916
US-09-864-761-3247
US-10-171-311-108
US-10-132-585-6615
US-10-059-397A-56
US-10-472-928-4979
B US-10-472-928-4979
B US-10-027-632-36171
US-10-027-632-36171
US-10-027-632-36191
US-10-027-632-297054
US-10-027-632-297054
US-10-027-632-297054
US-10-027-632-297054
US-10-027-632-139334
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
61.5%; Score 24.6; DB 6;
Best Local Similarity 76.9%; Pred. No. 2.1;
Matches 30; Conservative 0; Mismatches 9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 ATCCAGATTCTTGGCGGTAGAGAGCTGCTTGGTCAGACT
                                                                                                                                                                                                                                                                                                                                                                                        ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; LOCATION: (1096)
; OTHER INFORMATION: N = A, C, G, OR T/U
US-10-080-381B-1
FEATURE:
NAME/KEY: modified_base
```

```
APPLICANT:
                       셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Š
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Сарв
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Graham, James R.
APPLICANT: Graham, James R.
APPLICANT: Graham, James R.
APPLICANT: Genetics Institute, Inc.
TITLE OF INVENTION: POLYNUCLEOTIDES ENCODING NOVEL SECRETED PROTEINS
FILE REFERENCE: G1N 6400
CURRENT APPLICATION NUMBER: US/09/822,846
CURRENT FILING DATE: 2001-03-29
PRIOR PIPLICATION NUMBER: 60/195,605
PRIOR FILING DATE: 2000-04-06
NUMBER OF SEQ ID NOS: 629
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 554
LENGTH: 860
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61.5%; Score 24.6; DB 6; Length 1640; 76.9%; Pred. No. 2.2; 1ve 0; Mismatches 9; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 80.0%; Pred. No. 4.4;
Matches 28; Conservative 0; Mismatches 7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1277 Arccrearrerreccearacacaacaccreccacacr 1315
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 ATCCAGATTCTTGGCGGTAGAGAGCTGCTTGGTCAGACT 39
              CURRENT APPLICATION NUMBER: US/10/080,381B
CURRENT FILING DATE: 2002-02-19
PRIOR APPLICATION NUMBER: 60/291,354
PRIOR PILING DATE: 2001-05-15
PRIOR APPLICATION NUMBER: 60/274,706
PRIOR PILING DATE: 2001-03-09
PRIOR PILING DATE: 2001-03-09
PRIOR PILING DATE: 2001-03-09
PRIOR PILING DATE: 2001-03-09
NUMBER OF SEQ ID NOS: 75
SOFTWARE: PATENTIN VET: 2.1
                                                                                                                                                                                                                                                                                                                                                            NAME/KEY: modified base
LOCATION: (4)..(1628)
CSTHER INFORMATION: N = A, C, G, T or U
US-10-080-3818-67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Merberg, David
Treacy, Maurica
Agostino, Michael J.
Steininger II, Robert J.
Bowman, Michael R.
Spaulding, Vikki
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 554, Application US/09822846
Publication No. US20030027139A1
GENERAL INFORMATION:
APPLICANT: Jacobs, Kenneth
APPLICANT: McCoy, John M.
APPLICANT: LaVallie, Edward R.
APPLICANT: Collins-Racie, Lisa A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Howes, Steven H.
Resnick, Richard J.
Gulukota, Kamalakar
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 76.9 Matches 30; Conservative
FILE REFERENCE: UTSD:773US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Evans, Cheryl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Clark, Hilary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Fechtel, Kim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 3
US-09-822-846-554/c
                                                                                                                                                                                                                                                                                             TYPE: DNA
ORGANISM: RAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-09-822-846-554
                                                                                                                                                                                                                                                SEQ ID NO 67
LENGTH: 1640
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ద
```

```
Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Graham, James R.
APPLICANT: Genetics Institute, Inc.
TITLE OF INVENTION: POLYNUCLEOTIDES ENCODING NOVEL SECRETED PROTEINS
FILE REFERENCE: GIN 6400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ó
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Squence 616, Application US/10264049; Squence 616, Application No. US20040005579A1; Bublication No. US20040005579A1; GENERAL INFORMATION:

APPLICANT: Birse et al.; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies FILE REFERENCE: PA133P1; CURRENT APPLICATION NUMBER: US/10/264,049; CURRENT FILING DATE: 2002-10-04; PRIOR APPLICATION NUMBER: PCT/US01/18569; PRIOR APPLICATION NUMBER: US 60/209,467; PRIOR FILING DATE: 2000-06-07; NUMBER OF SEQ ID NOS: 4360; SOFTWARE: Patentin Ver. 3.1; SEQ ID NO 616.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 23.8; DB 3; Length 1928;
Pred. No. 4.9;
0; Mismatches 7; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           176 Arccaarrcrreedecraedargrecrrrrea 142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 ATCCAGATTCTTGGCGGTAGAGAGCTGCTTGGTCA 35
55 Arccaparrerresecerasesargreerrrrea 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION NUMBER: US/09/822,846
CURRENT FILING DATE: 2001-03-29
PRIOR PILING DATE: 2000-04-06
NUMBER OF SEQ ID NOS: 629
SOFTWARE: Patentin Ver. 2.0
LENGTH: 1928
                                                                                                                                                                                       APPLICANT: Jacobs, Kenneth
APPLICANT: McCoy, John M.
APPLICANT: McCoy, John M.
APPLICANT: LaVallie, Edward R.
APPLICANT: Evans, Cheryl
APPLICANT: Evans, Cheryl
APPLICANT: Merberg David
APPLICANT: Agostino, Michael J.
APPLICANT: Spanlding, Wichael R.
APPLICANT: Spanlding, Vikki
APPLICANT: Won, Gordon G.
APPLICANT: Won, Gordon G.
                                                                                                                 Sequence 570, Application US/09822846 Publication No. US20030027139A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gulukota, Kamalakar
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Howes, Steven H.
Resnick, Richard J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 59.5%;
Best Local Similarity 80.0%;
Matches 28; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Clark, Hilary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Fechtel, Kim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: DNA ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-10-264-049-616/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-09-822-846-570
```

ô

ö

Gaps

ö

1 ATCCAGATTCTTGGCGGTAGAGAGCTGCTTGGTCA 35

```
Query Match 59.5%; Score 23.8; DB 7; Length 7747; Best Local Similarity 80.0%; Pred. No. 5.9; Matches 28; Conservative 0; Mismatches 7; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TITLE OF INVENTION: No. US20030104413A1e1 Nucleic Acids and ITILE OF INVENTION: Polypeptides; FILE REPERDER: 789CIP2BCON CURRENT APPLICATION NUMBER: US/10/119,926; CURRENT FILING DATE: 2002-04-09; FRIOR PEDLICATION NUMBER: 09/574,454; PRIOR FILING DATE: 2000-05-19; PRIOR FILING DATE: 2000-05-19; PRIOR FILING DATE: 2000-05-19; PRIOR FILING DATE: 2000-03-07; NUMBER: OF SEQ ID NOS: 108; SEQ ID NO 21.

LENGTH: 7827
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               59.5%; Score 23.8; DB 5; Length 7827;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          5983 Arccaaarrcirececraecearerecrirrica 5949
                   FILE KEFERANIE: 412.043
CURRENT FILING DATE: 2002-09-06
PRIOR PILING DATE: 2002-09-06
PRIOR PILING DATE: 2002-09-06
PRIOR PILING DATE: 2000-09-19
PRIOR PILING DATE: 2000-07-14
PRIOR PILING DATE: 2000-07-14
PRIOR PILING DATE: 2000-06-17
PRIOR PILING DATE: 2000-06-17
PRIOR PILING DATE: 2000-06-19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 21, Application US/10119926
Publication No. US20030104413A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Yang, Yonghong
Xue, Aidong J.
Drmanac, Radoje T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Tang, Y. Tom
APPLICANT: Liu, Chenghua
APPLICANT: Asundi, Vinod
APPLICANT: Asundi, Vinod
APPLICANT: Ren, Peiyan
APPLICANT: Chao, Qing A.
APPLICANT: Chen, Rui-hong
APPLICANT: Wehrman, Tom
APPLICANT: Zhou, Ping
APPLICANT: Zhou, Ping
APPLICANT: Zhou, Ping
APPLICANT: Zhou, Ping
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; NAME/KEY: CDS
; LOCATION: (121)..(7497)
US-10-119-926-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: DNA ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; NAME/KEY: CDS
; LOCATION: (41)..(7414)
US-10-221-278-69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-10-119-926-21/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 69, Application US/10291172
| Bublication No. US20030228584A1
| GENERAL INFORMATION:
| APPLICANT: Hyseq, Inc
| TITLE OF INVENTION: No. US20030228584A1e1 Nucleic Acids and Polypeptides
| FILE REFRENCE: 2172-045
| FILE OF INVENTION NUMBER: US/10/291,172
| CURRENT FILING DATE: 2000-11-08
| PRIOR APPLICATION NUMBER: 09/663,367
| PRIOR APPLICATION NUMBER: 09/665,363
| PRIOR FILING DATE: 2000-00-19
| PRIOR FILING DATE: 2000-00-14
| PRIOR FILING DATE: 2000-00-14
| PRIOR FILING DATE: 2000-00-17
| PRIOR FILING DATE: 2000-06-17
| PRIOR FILING DATE: 2000-06-17
| PRIOR FILING DATE: 2000-06-17
| PRIOR FILING DATE: 2000-06-19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          10-10-21-278-69/c

Sequence 69, Application US/10221278

Publication No. US20040034208A1

GENERAL INFORMATION:

APPLICANT: Hyaeq, Inc

TITLE OF INVENTION: No. US20040034208A1el Nucleic Acids and Polypeptides
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 59.5%; Score 23.8; DB 6; Length 3134; Best Local Similarity 80.0%; Pred. No. 5.2; Matches 28; Conservative 0; Mismatches 7; Indels 0.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 23.8; DB 6; Length 7747;
Pred. No. 5.9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1330 Arccaaarrcrreececraeeearerecrrrrca 1296
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           5983 Arccaaarrcrrccccaacaacaarcrcrrrrca 5949
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 ATCCAGATTCTTGGCGGTAGAGAGCTGCTTGGTCA 35
                                                                               NAME/KEY: misc feature

LOCATION: (3108)...(3108)

OTHER INFORMATION: n equals a,t,g, or c
FEATURE:
NAME/KEY: misc feature
LOCATION: (3117)...(3117)

OTHER INFORMATION: n equals a,t,g, or c
FEATURE:
NAME/KEY: misc feature
LOCATION: (3132)...(3132)

COTHER INFORMATION: n equals a,t,g, or c
US-10-264-049-616
LOCATION: (319)..(319)
OTHER INFORMATION: n equals a,t,g,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     59.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Local Similarity 80.0
Matches 28; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; NAME/KGY: CDS
; LOCATION: (41)..(7414)
US-10-291-172-69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 6
US-10-291-172-69/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
```

ö

ö

Gaps

ö

```
Length 7827;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 9; Length 7827;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                6063 Arccharrcrrececraecarerecrrrrren 6029
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          6063 Arccanarrerreseserasesarereerrerea 6029
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 ATCCAGATTCTTGGCGGTAGAGAGCTGCTTGGTCA 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
APPLICANT: Tang, Y. Tom
APPLICANT: Tang, Y. Tom
APPLICANT: Tang, Y. Tom
APPLICANT: Asundi, Vinod
APPLICANT: Ren, Feiyan
APPLICANT: Ren, Feiyan
APPLICANT: Ren, Feiyan
APPLICANT: Ren, Feiyan
APPLICANT: Pananac, Radoje T.
ITLE OF INVENTION: Novel Nucleic Acids and
ITLE OF INVENTION: Polypeptides
FILE REFERENCE: 784C1P2BDV3
FILE REFERENCE: 784C1P2BDV3
CURRENT APPLICATION NUMBER: US/10/122,851
CURRENT FILING DATE: 2000-04-12
PRIOR FILING DATE: 2000-04-25
PRIOR APPLICATION NUMBER: 09/468,725
PRIOR APPLICATION NUMBER: 09/488,725
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            59.5%; Score 23.8; Di
80.0%; Pred. No. 5.9;
tive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 59.5%; Score 23.8; D
Best Local Similarity 80.0%; Pred. No. 5.9;
Matches 28; Conservative 0; Mismatches
                      PRIOR APPLICATION NUMBER: 09/620,312
PRIOR FILING DATE: 2000-07-19
PRIOR PLING DATE: 2000-04-25
PRIOR FILING DATE: 2000-04-25
PRIOR FILING DATE: 2000-04-25
PRIOR PLING DATE: 2000-01-21
NUMBER OF SEQ ID NOS: 1104
SOFTWARE: pt_Ft_genes Version 1.0
SEQ ID NO 104
LENGTH: 7827
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 104, Application US/10122851
Publication No. US20050239060A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-10-210-172-35/c; Sequence 35, Application US/10210172; Publication No. US20040043928A1; GENERAL INFORMATION:
  2002-04-04
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity 80.0
1es 28; Conservative
                                                                                                                                                                                                                                                                                                                                               ; FEATURE:
; NAME/KEY: CDS
; LOCATION: (121)..(7497)
US-10-117-722-104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; NAME/KEY: CDS
; LOCATION: (121)..(7497)
US-10-122-851-104
                                                                                                                                                                                                                                                                                             TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-10-122-851-104/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local S:
Matches 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                              ö
                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 104, Application US/10117722
; Sequence 104, Application US/10117722
; Publication No. US20030219744A1
; GENERAL INFORMATION:
; APPLICANT: Tang, Y. Tom
; APPLICANT: Asundi, Vinod
; APPLICANT: Asundi, Vinod
; APPLICANT: Drmanac, Radoje T.
; TITLE OF INVENTION: No. US20030219744A1e1 Nucleic Acids and
; TITLE OF INVENTION: Polypeptides
; TITLE OF INVENTION: 1961/Peptides
; FILE REFERENCE: 784CIP2BGIP
; CURRENT APPLICATION NUMBER: US/10/117,722
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 23.8; DB 5; Length 7827;
Pred. No. 5.9;
0; Mismatches 7; Indels 0
                           Indels
                        7;
                                                                                                                               6063 Arccharrcrrececraecenerererrrren 6029
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             6063 ATCCAAATTCTTGGCGCTAGGGATGTGCTTTTTCA 6029
                                                                             1 ATCCAGATTCTTGGCGGTAGAGAGCTGCTTGGTCA 35
Pred. No. 5.9;
0; Mismatches
                                                                                                                                                                                                                                                               Sequence 104, Application US/10037270 Publication No. US20030104529A1 GENERAL INFORMATION:
Best Local Similarity 80.0%;
Matches 28; Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 59.5%;
Best Local Similarity 80.0%;
Matches 28; Conservative (
                                                                                                                                                                                                                                                                                                                                          APPLICANT: Tang, Y. Tom
APPLICANT: Tang, Y. Tom
APPLICANT: Asundi, Vinod
APPLICANT: Zhang, Jie
APPLICANT: Chen, Rui-hong
APPLICANT: Chen, Rui-hong
APPLICANT: Zhao, Qing A.
APPLICANT: Xue, Aidong J.
APPLICANT: Xue, Aidong J.
APPLICANT: Yang, Yonghong
APPLICANT: Yang, Yonghong
APPLICANT: Zhou, Ping
APPLICANT: Mang, Jian-Rui
APPLICANT: Mang, Jian-Rui
APPLICANT: Wang, Ding
APPLICANT: Wang, Ding
APPLICANT: Wang, Zhiwei
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; NAME/KEY: CDS
; LOCATION: (121)..(7497)
US-10-037-270-104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                           US-10-037-270-104/c
                                                                                                                               g
                                                                                ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              셤
```

ö

Gaps

```
RESULT 14

US-10-501-282-995/c

i Gequence 995, Application US/10501282

sequence 995, Application Wol10501282

sequence 995, Application Wol1050203280A1

GENERAL INFORMATION:
APPLICANT: MCHICHALL, JOHN CALHOUN
APPLICANT: EAGINERY, ROBERT JOHN
APPLICANT: EAGINERY, LEAH DIANE
ITILE OF INVENTION: ALLOJOCOCCUS OTITIDIS OPEN READING FRAMES (ORFS) ENCODING
ITILE OF INVENTION: ALLOJOCOCCUS OTITIDIS OPEN READING FRAMES (ORFS) ENCODING
ITILE OF INVENTION: ALLOJOCOCCUS OTITIDIS OPEN READING FRAMES (ORFS)
FILE REFERENCE: AMI00780 L2

CURRENT PELLOGICATION NUMBER: 60/333,777

PRIOR PELLOGICATION NUMBER: 60/333,777

PRIOR PELLOGICATION NUMBER: 60/333,777

PRIOR APPLICATION NUMBER: 60/333,777

PRIOR APPLICATION NUMBER: PCT/US02/36123

PRIOR PELLOR APPLICATION NUMBER: PCT/US02/36123

PRIOR PLING DATE: 2002-11-25

SEQ ID NO 955

LENGTH: 1266

PRIOR PLENGTH: 1266
                                                                                                                  Sequence 24140, Application US/10369493

Publication No. US20030233675A1

GENERAL INPORMATION:

APPLICANT: Hinkle, Gregory J.

APPLICANT: Blater, Steven C.

APPLICANT: Goldman, Barry S.

CURRENT APPLICATION NUMBER: US/10/369,493

CURRENT APPLICATION NUMBER: US 60/360,039

PRIOR APPLICATION NUMBER: US 60/360,039

PRIOR FILING DATE: 2003-02-21

NUMBER OF SEQ ID NOS: 47374

SEQ ID NO 24140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Guery Match

59.0%; Score 23.6; DB 6; Length 2157;

Best Local Similarity 76.3%; Pred. No. 6.1;

Matches 29; Conservative 0; Mismatchem 9. Twall
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 9; Length 1266;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indela
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        399 ATCCAGATTCATCGCCTTAATGATCGCTTGATCAGAC 362
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 ATCCAGATICITGGCGGTAGAGAGCTGCTTGGTCAGAC 38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ..
..
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   915 AAATTGTTGGAGGTAGCTAGCTGCTTGGTCA 885
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 23, DB 9
Pred. No. 10;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     S AGATICITGGCGGTAGAGAGCTGCTTGGTCA 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; TYPE: DNA; Cenorhabdus nematophilus
; ORGANISM: Xenorhabdus nematophilus
US-10-369-493-24140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPB: DNA ORGANISM: Alloiococcus otitidis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 57.5%;
Best Local Similarity 83.9%;
Matches 26; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; NAME/KRY: CDS
; LOCATION: (121)..(1263)
US-10-501-282-995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Malyankar, Uriel
APPLICANT: MacDougall, John
APPLICANT: MacDougall, John
APPLICANT: Stone, David
APPLICANT: Lepley, Denise et al.
TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME, AND METHOD
FILE REFERENCE: 21402-416 A
CURRENT PELLING DATE: 2001-08-01
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION NUMBER: 60/309, 501

PRIOR PLING DATE: 2001-08-02

PRIOR PILING DATE: 2001-08-02

PRIOR PILING DATE: 2001-09-03

PRIOR PILING DATE: 2001-09-04-19

PRIOR PILING DATE: 2001-09-11

PRIOR PLING DATE: 2001-04-19

PRIOR PILING DATE: 2001-04-19

PRIOR PILING DATE: 2001-08-03

PRIOR PILING DATE: 2001-08-03

PRIOR PILING DATE: 2001-08-03

PRIOR PILING DATE: 2001-08-07

PRIOR PLING DATE: 2001-08-07

PRIOR PILING DATE: 2001-08-17

PRIOR SPEING PRIOR APPLICATION NUMBER: 60/312,892

PRIOR PILING DATE: 2001-08-17

PRIOR PILING DATE: 2001-08-17

PRIOR PILING DATE: 2001-08-17

PRIOR APPLICATION NUMBER: 60/312,892

PRIOR PILING DATE: 2001-08-17

PRIOR APPLICATION NUMBER: 60/312,892

PRIOR PILING DATE: 2001-08-16

PRIOR PILING DATE: 2001-08-17

PRIOR PILING DATE: 2001-08-17

PRIOR PILING DATE: 2001-08-17

PRIOR PILING DATE: 2001-08-17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 7; Length 9508;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 ATCCAGATTCTTGGCGGTAGAGAGCTGCTTGGTCA 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 23.8; DB
Pred. No. 6;
0; Mismatches
                                                                                                                                                                                                Li, Li
Ji, Weizhen
Padigaru, Muralidhara
Casman, Stacie
'OSS', Edward
'! Boldog, Perenc
'T: Gorman, Linda
'NT: Leite, Mario
'NT: Vernet, Corine
ANT: Anderson, David
Guo, Xiaojia
                                                                                                                  Rieger, Daniel
Shimkets, Richard
Zerhusen, Bryan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   59.5%;
                             Miller, Charles
Patturajan, Meera
Pena, Carol
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Hjalt, Tord
Rastelli, Luca
Spytek, Kimberly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gerlach, Valerie
Hjalt, Tord
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Edinger, Shlomit
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 59.5
Best Local Similarity 80.0
Matches 28; Conservative
Kekuda, Ramesh
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; LOCATION: (170)..(9187)
US-10-210-172-35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME/KEY: CDS
APPLICANT
```

ઠ

```
RESULT 15
US-10-501-282-997/C
i Sequence 997/C
i Deblication No. US20050203280Al
i GENERAL INFORMATION:
APPLICANT: MACHICHEL, JOHN CALHOUN
APPLICANT: ZAGTRSKY, ROBERT JOHN
TITLE OF INVENTION: DALLOIOCOCCUS OTITIDIS OPEN READING FRAMES (ORPS) ENCODING
TITLE OF INVENTION: PLYPEPTIDE ANTIGENS, IMMUNOGENIC COMPOSITIONS AND USES THEREOF
FILE REFERENCE: AM100780 L2
CURRENT APPLICATION NUMBER: US/10/501,282
CURRENT FILING DATE: 2004-11-29
PRIOR FILING DATE: 2002-11-18
PRIOR PLILING DATE: 2002-11-18
PRIOR PLILING DATE: 2002-11-25
SPRIOR APPLICATION NUMBER: 60/426,742
PRIOR PLILING DATE: 2002-11-25
SPRIOR APPLICATION NUMBER: 9CT/US02/36123
PRIOR PLILING DATE: 2002-11-25
SOUTHARE: Patentin version 3.2
SOUTHARE: Patentin version 3.2
SEQ ID NO 997
LEMCTH: 1266
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  °
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 57.5%; Score 23; DB 9; Length 1266; Best Local Similarity 83.9%; Pred. No. 10; Matches 26; Conservative 0; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        915 AAATTGTTGGAGGTAGCTAGCTGCTTGGTCA 885
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        5 AGATICITGGCGGTAGAGAGCTGCTTGGTCA 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: DNA ORGANISM: Alloiococcus otitidis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; FEATURE:
; NAME/KEY: CDS
; LOCATION: (25)..(1263)
US-10-501-282-997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   g
```

Search completed: April 18, 2006, 23:13:57 Job time : 680.5 secs

```
Wed Apr 19 09:00:17 2006
```

```
   0.0
   0.0
   0.0
   0.0
   0.0
   0.0
   0.0
   0.0
   0.0
   0.0
   0.0
   0.0
   0.0
   0.0
   0.0
   0.0
   0.0
   0.0
   0.0
   0.0
   0.0
   0.0
   0.0
   0.0
   0.0
   0.0
   0.0
   0.0
   0.0
   0.0
   0.0
   0.0
   0.0
   0.0
   0.0
   0.0
   0.0
   0.0
   0.0
   0.0
   0.0
   0.0
   0.0
   0.0
   0.0
   0.0
   0.0
   0.0
   0.0
   0.0
   0.0
   0.0
   0.0
   0.0
   0.0
   0.0
   0.0
   0.0
   0.0
   0.0
   0.0
   0.0
   0.0
   0.0
   0.0
   0.0
   0.0
   0.0
   0.0
   0.0
   0.0
   0.0
   0.0
   0.0
   0.0
   0.0
   0.0
   0.0
   0.0
   0.0
   0.0
   0.0
   0.0
   0.0
   0.0
   0.0
   0.0
   0.0
   0.0
   0.0
   0.0
   0.0
   0.0
   0.0
   0.0
   0.0
   0.0
   0.0
   0.0
   0.0
   0.0
   0.0
   0.0
   0.0
   0.0
   0.0
   0.0
   0.0
   0.0
   0.0
   0.0
   0.0
   0.0
   0.0
   0.0
   0.0
   0.0
   0.0
   0.0
   0.0
   0.0
   0.0
   0.0
   0.0
   0.0
   0.0
   0.0
   <t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 2
US-09-925-065A-918089
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 1
US-11-136-527-2411/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Wyeth
                                                                                                                                                                                                                                                                                     셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 2411, Ap
Sequence 918089,
Sequence 591215,
Sequence 591216,
Sequence 10681, A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 624090,
Sequence 1298016,
Sequence 1091533,
Sequence 411990,
Sequence 411990,
Sequence 48123, A
Sequence 78123, A
Sequence 787534,
                                                                                                                                                                              April 18, 2006, 19:49:40; Search time 352 Seconds (without alignments) 457.708 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Description
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Published Applications NA New:*

| SIDSS/ptodata/2/pubpna/US08_NEW_PUB.seq:*
| SIDSS/ptodata/2/pubpna/US08_NEW_PUB.seq:*
| SIDSS/ptodata/2/pubpna/US07_NEW_PUB.seq:*
| SIDSS/ptodata/2/pubpna/PCT_NEW_PUB.seq:*
| SIDSS/ptodata/2/pubpna/US09_NEW_PUB.seq:*
| SIDSS/ptodata/2/pubpna/US09_NEW_PUB.seq:*
| SIDSS/ptodata/2/pubpna/US09_NEW_PUB.seq:*
| SIDSS/ptodata/2/pubpna/US10_NEW_PUB.seq:*
| SIDSS/ptodata/2/pubpna/US10_NEW_PUB.seq:*
| SIDSS/ptodata/2/pubpna/US10_NEW_PUB.seq:*
| SIDSS/ptodata/2/pubpna/US11_NEW_PUB.seq:*
                      GenCore version 5.1.7
Copyright (c) 1993 - 2006 Biocceleration Ltd.
                                                                                                                                                                                                                                                                                                                                               1 atccagattcttggcggtagagagctgcttggtcagactt 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  4 US-11-136-527-2411

US-09-925-065A-918089

US-09-925-065A-591215

US-09-925-065A-591216

US-10-301-480-10681

US-10-301-480-10681

US-10-301-480-1208016

US-10-301-480-1208016

US-10-301-480-1208016

US-10-301-480-1208016

US-10-301-480-1208016

US-10-301-480-1990

US-10-925-065A-411990

US-10-750-185-48123

US-10-750-185-48123

US-10-925-065A-715734

US-11-000-463-507

US-11-000-463-508

US-11-000-463-36

US-11-000-463-36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               9281099 seqs, 2013915447 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                  OM nucleic - nucleic search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                                Gapop 10.0 , Gapext 0.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB seq length: 0
DB seq length: 200000000
                                                                                                                                                                                                                                                                                        SEQ4-THEN-SEQ3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query
Match Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          640
1073
1073
1379
                                                                                                                                                                                                                                                                                                                                                                                                    IDENTITY NUC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     50.05

50.05

50.05

50.05

50.05

50.05

50.05

50.05

50.05

50.05

50.05

50.05

50.05

50.05

50.05

50.05

50.05

50.05

50.05

50.05

50.05

50.05

50.05

50.05

50.05

50.05

50.05

50.05

50.05

50.05

50.05

50.05

50.05

50.05

50.05

50.05

50.05

50.05

50.05

50.05

50.05

50.05

50.05

50.05

50.05

50.05

50.05

50.05

50.05

50.05

50.05

50.05

50.05

50.05

50.05

50.05

50.05

50.05

50.05

50.05

50.05

50.05

50.05

50.05

50.05

50.05

50.05

50.05

50.05

50.05

50.05

50.05

50.05

50.05

50.05

50.05

50.05

50.05

50.05

50.05

50.05

50.05

50.05

50.05

50.05

50.05

50.05

50.05

50.05

50.05

50.05

50.05

50.05

50.05

50.05

50.05

50.05

50.05

50.05

50.05

50.05

50.05

50.05

50.05

50.05

50.05

50.05

50.05

50.05

50.05

50.05

50.05

50.05

50.05

50.05

50.05

50.05

50.05

50.05

50.05

50.05

50.05

50.05

50.05

50.05

50.05

50.05

50.05

50.05

50.05

50.05

50.05

50.05

50.05

50.05

50.05

50.05

50.05

50.05

50.05

50.05

50.05

50.05

50.05

50.05

50.05

50.05

50.05

50.05

50.05

50.05

50.05

50.05

50.05

50.05

50.05

50.05

50.05

50.05

50.05

50.05

50.05

50.05

50.05

50.05

50.05

50.05

50.05

50.05

50.05

50.05

50.05

50.05

50.05

50.05

50.05

50.05

50.05

50.05

50.05

50.05

50.05

50.05

50.05

50.05

50.05

50.05

50.05

50.05

50.05

50.05

50.05

50.05

50.05

50.05

50.05

50.05

50.05

50.05

50.05

50.05

50.05

50.05

50.05

50.05

50.05

50.05

50.05

50.05

50.05

50.05

50.05

50.05

50.05

50.05

50.05

50.05

50.05

50.05

50.05

50.05

50.05

50.05

50.05

50.05

50.05

50.05

50.05

50.05

50.05

50.05

50.05

50.05

50.05

50.05

50.05

50.05

50.05

50.05

50.05

50.05

50.05

50.05

50.05

50.05

50.05

50.05

50.05

50.05

50.05

50.05

50.05

50.05

50.05

50.05

50.05

50.05

50.05

50.05

50.05

50.05

50.05

50.05

50.05

50.05

50.05

50.05

50.05

50.05

50.05

50.05

50.05

50.05

50.05

50.05

50.05

50.05

50.05

50.05

50.05

50.05

50.05

50.05

50.05

50.05

50.05

50.05

50.05

50.05

50.05

50.05

50.05

50
                                                                                                                                                                                                                                                                                           Title:
Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Scoring table:
                                                                                                                                                                                                                                                                                                                                                  Sequence:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Database
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Minimum I
Maximum I
                                                                                                                                                                                       Run on:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Result
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Š
```

00000000

```
Sequence 219, App
Sequence 194, App
Sequence 50135,
Sequence 25101, A
Sequence 43843, A
Sequence 43843, A
Sequence 62181, A
Sequence 6218, A
Sequence 60125,
Sequence 608235,
Sequence 608235,
Sequence 608236,
Sequence 355591,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 34935, A Sequence 34935, A Sequence 690684, Sequence 189, App Sequence 167, App Sequence 25010, A Sequence 25010, A Sequence 25010, A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Mounte, William M
TITLE OF INVENTION: Probe Arrays For Expression Profiling of Rat Genes
FILE REFERENCE: 031896-041000 (AMI01086)
CURRENT APPLICATION NUMBER: US/11/136,527
CURRENT FILING DATE: 2005-05-25
PRIOR APPLICATION NUMBER: US 60/574,294
PRIOR PILING DATE: 2005-05-36
NUMBER OF SEQ ID NOS: 362830
SOFTWARE: Patentin version 3.2
SEQ ID NO 2411
LENGTH: 1706
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                          Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 918089, Application US/09925065A
Publication No. US20040181048A1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single
TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
FILE REFERENCE: 108627.135
CURRENT APPLICATION NUMBER: US/09/925,065A
CURRENT FILING DATE: 2001-08-08
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 1706;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                             4 US-11-124-367A-194
US-09-925-065A-508353
US-10-750-185-26101
US-10-750-623-26101
US-10-750-623-43843
US-10-750-623-43843
US-10-995-561-69138
US-10-995-561-69145
US-10-995-561-69145
US-09-925-065A-608235
US-09-925-065A-608236
US-10-301-480-427081
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-10-750-185-34935
US-10-750-623-34935
US-10-9-925-065A-690684
US-11-120-308-189
US-11-031-206-167
US-10-995-561-11406
US-10-301-480-126247
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-09-925-065A-355591
US-09-925-065A-697463
US-11-031-206-165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             428 ccacarregecececeseaecrerecriecreaea 394
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3 CCAGATTCTTGGCGGTAGAGAGCTGCTTGGTCAGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 22.2; DE Pred. No. 22; 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 2411, Application US/11136527
Publication No. US20050287570A1
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 55.5%;
Best Local Similarity 77.1%;
Matches 27; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; TYPE: DNA
; ORGANISM: Rattus norvegicus
US-11-136-527-2411
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1059
1059
2837
3202
3236
23803
543
114884
115084
115084
115084
12080
12090
12090
12090
12090
12090
12090
12090
12090
12090
12090
12090
12090
12090
12090
12090
12090
12090
12090
12090
12090
12090
12090
12090
12090
12090
12090
12090
12090
12090
12090
12090
12090
12090
12090
12090
12090
12090
12090
12090
12090
12090
12090
12090
12090
12090
12090
12090
12090
12090
12090
12090
12090
12090
12090
12090
12090
12090
12090
12090
12090
12090
12090
12090
12090
12090
12090
12090
12090
12090
12090
12090
12090
12090
12090
12090
12090
12090
12090
12090
12090
12090
12090
12090
12090
12090
12090
12090
12090
12090
12090
12090
12090
12090
12090
12090
12090
12090
12090
12090
12090
12090
12090
12090
12090
12090
12090
12090
12090
12090
12090
12090
12090
12090
12090
12090
12090
12090
12090
12090
12090
12090
12090
12090
12090
12090
12090
12090
12090
12090
12090
12090
12090
12090
12090
12090
12090
12090
12090
12090
12090
12090
12090
12090
12090
12090
12090
12090
12090
12090
12090
12090
12090
12090
12090
12090
12090
12090
12090
12090
12090
12090
12090
12090
12090
12090
12090
12090
12090
12090
12090
12090
12090
12090
12090
12090
12090
12090
12090
12090
12090
12090
12090
12090
12090
12090
12090
12090
12090
12090
12090
12090
12090
12090
12090
12090
12090
12090
12090
12090
12090
12090
12090
12090
12090
12090
12090
12090
12090
12090
12090
12090
12090
12090
12090
12090
12090
12090
12090
12090
12090
12090
12090
12090
12090
12090
12090
12090
12090
12090
12090
12090
12090
12090
12090
12090
12090
12090
12090
12090
12090
12090
12090
12090
12090
12090
12090
12090
12090
12090
12090
12090
12090
12090
12090
12090
12090
12090
12090
12090
12090
12090
12090
12090
12090
12090
12090
12090
12090
12090
12090
12090
12090
12090
12090
12090
12090
12090
12090
12090
12090
12090
12090
12090
12090
12090
12090
12090
12090
12090
12090
12090
12090
12090
12090
12090
12090
12090
12090
12090
12090
12090
12090
12090
12090
12090
12090
12090
12090
12090
12090
12090
12090
12090
12090
12090
12090
12090
12090
12090
12090
12090
12090
12090
12090
12090
12090
12090
12090
12090
12090
12090
12090
12090
12090
12090
12
```

```
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; ORGANISM: Homo sapien
US-10-301-480-10681
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-09-925-065A-591216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-10-301-480-10681
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; CENERAL INFORMATION:
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
; TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
; TITLE REFERENCE: 100827.135
; CURRENT APPLICATION NUMBER: US 60/243,096
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR PILING DATE: 2000-110-20
; PRIOR PILING DATE: 2000-111-20
; PRIOR PILING DATE: 2000-111-30
; PRIOR PILING DATE: 2000-111-30
; PRIOR PILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR PILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR PILING DATE: 2001-01-16
; PRIOR PILING DATE: 201-01-16
; PRIOR PILING DATE: 201-01-01-10
; PRIOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 591216, Application US/09925065A
Publication No. US20040181048A1
GENERAL INFORMATION:
APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single
TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 663;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 6; Length 518;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ę,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 53.5%; Score 21.4; DB 6; Best Local Similarity 80.6%; Pred. No. 41; Matches 25; Conservative 0; Mismatches 6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                235 dargerederderaadaacreceradacadacrir 269
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      6 GATTCTTGGCGGTAGAGAGCTGCTTGGTCAGACTT 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        540 rarritárésradadaccrederregreacer 570
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 20.6; DB Fred. No. 87; 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         9 TCTTGGCGGTAGAGAGCTGCTTGGTCAGACT 39
PRIOR APPLICATION NUMBER: US 60/243,096
PRIOR FILING DATE: 2000-10-24
PRIOR FILING DATE: 2000-11-20
PRIOR FILING DATE: 2000-11-20
PRIOR APPLICATION NUMBER: US 60/250,092
PRIOR APPLICATION NUMBER: US 60/260,092
PRIOR APPLICATION NUMBER: US 60/261,766
PRIOR FILING DATE: 2001-01-16
PRIOR FILING DATE: 2001-01-16
PRIOR FILING DATE: 2001-06-09
NUMBER OF SEQ ID NOS: 957086
SOFTWARE: PSELSEQ for Windows Version 4.0
SERVITH: 663
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-09-925-065A-591215; Sequence 591215, Application US/09925065A; Publication No. US20040181048A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 74.3%;
Matches 26; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; ORGANISM: Homo sapiens
US-09-925-065A-918089
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; ORGANISM: Homo sapiens
US-09-925-065A-591215
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 4
US-09-925-065A-591216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        원
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ठ
```

```
Sequence 10681, Application US/10301480
; Sequence 10681, Application US/10301480
; Publication No. US20060057564A1
; GENERAL INPORMATION:
GENERAL INPORMATION:
TITLE OF INVENTION: Identifiction and Mapping of Single Nucleotide Polymorphisms
TITLE OF INVENTION: in the Human Genome
TITLE OF INVENTION: 10822-11.27
; CURRENT PILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: US 10/215,598
; PRIOR PILING DATE: 2002-08-09
; PRIOR PLLING DATE: 2001-08-10
; PRIOR FILING DATE: 2001-08-10
; PRIOR FILING DATE: 2001-08-10
; NUMBER OF SEQ ID NOS: 1226818
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 10681
; LENGTH: 535
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-10-301-480-624090

| Sequence 624090, Application US/10301480
| Sequence 624090, Application US/20060057564A1
| Publication No. US20060057564A1
| GENERAL INFORMATION:
| APPLICANT' WANG, David G.
| TITLE OF INVENTION: Identifiction and Mapping of Single Nucleotide Polymorphisms
| TITLE OF INVENTION: in the Human Genome
| FILE REPRESENCE: 10822'.137
| CURRENT APPLICATION NUMBER: US/10/301,480
| CURRENT FILING DATE: 2002-11-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gape
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match

51.5%; Score 20.6; DB 6; Length 535;
Best Local Similarity 74.3%; Pred. No. 87;
Matches 26; Conservative 0; Mismatches 9; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 535;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 20.6; DB 9;
Pred. No. 87;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  245 cargerecerataacacereceracacacacer 279
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          245 dangenegenegnaakakeneenegaeken 279
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            6 GATTCTTGGCGGTAGAGAGCTGCTTGGTCAGACTT
CURRENT PELLING DATE: 2001-08-08

CURRENT FILING DATE: 2001-08-08

PRIOR PELLING DATE: 2001-08-08

PRIOR FILING DATE: 2000-10-24

PRIOR FILING DATE: 2000-10-24

PRIOR FILING DATE: 2000-11-20

PRIOR FILING DATE: 2000-11-30

PRIOR FILING DATE: 2000-11-30

PRIOR FILING DATE: 2000-11-30

PRIOR FILING DATE: 2000-11-30

PRIOR FILING DATE: 2001-01-16

PRIOR PILING DATE: 2001-01-16

PRIOR PILING DATE: 2001-01-16

PRIOR PILING DATE: 2001-01-16

PRIOR FILING DATE: 2001-05-09

NUMBER OF SEQ ID NOS: 957086

SOFTWARE: PSECSEQ for Windows Version 4.0

SENGTH: 535
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 74.3%;
Matches 26; Conservative
```

ö

a ઠે

```
Sequence 1091533, Application US/10301480

Sequence 1091533, Application US/10301480

Sequence 1091533, Application US. US20060057564A1

GENERAL INFORMATION:

SENDICANT: Wang, David G.

TITLE OF INVENTION: In the Human Genome

PILE REFERENCE: 108427.137

CURRENT FILING DATE: 2002-11-21

PRIOR APPLICATION NUMBER: US 60/311,695

PRIOR APPLICATION NUMBER: US 60/311,695

PRIOR APPLICATION NUMBER: US 60/311,695

PRIOR PILING DATE: 2001-08-10

NUMBER OF SEQ ID NOS: 1226818

SOFTWARE: PSESEE FOR Windows Version 4.0

SEQ ID NO 1091533
                                                                                                                                                                                                                                                                                                                                             Sequence 478124, Application US/10301480

Sequence 478124, Application US/10301480

Sequence 478124, Application US. US2006057564A1

GENERAL INFORMATION:

JENERAL INFORMATION:

TITLE OF INVENTION: Identifiction and Mapping of Single Nucleotide Polymorphisms

TITLE OF INVENTION: 1n the Human Genome

TITLE OF INVENTION: 1n the Human Genome

TITLE OF INVENTION: 1n the Human Genome

FILE REFERENCE: 10827.1137

CURRENT PAPLICATION NUMBER: US/10/301,480

CURRENT FILING DATE: 2002-11-21

PRIOR APPLICATION NUMBER: US 60/311,695

PRIOR APPLICATION NUMBER: US 60/311,695

PRIOR PILING DATE: 2001-08-10

NUMBER OF SEQ ID NOS: 1226818

SOFTWARE: FeatSEQ for Windows Version 4.0

SEQ ID NO 4781124

LENGTH: 592
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                DB 10; Length 557;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 592;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 592;
                                                                                                                                   Indele
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                              9.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             9
                                                                                                                                                                                                                                    167 garrarregracagagrecrectregraacrerr 201
                                                                                                                                                                                       40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               49 GATAATTTGCAGGAAAGAGCAACTTTGTCAGACTT
                                                                                                                                                                                       6 GATTCTTGGCGGTAGAGAGCTGCTTGGTCAGACTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   6 GATTCTTGGCGGTAGAGACTGCTTGGTCAGACTTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           6 GATICITGGCGGTAGAGAGCTGCTTGGTCAGACTT
                                                                                Query Match
51.5%; Score 20.6; D
Best Local Similarity 74.3%; Pred. No. 88;
Matches 26; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 51.5%; Score 20.6; D
Best Local Similarity 74.3%; Pred. No. 89;
Matches 26; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Sest Local Similarity 74.3%; Pred. No. 89;
Matches 26; Conservative 0; Mismatches
     ; ORGANISM: Homo sapien
US-10-301-480-1208016
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; ORGANISM: Homo sapien
US-10-301-480-478124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; ORGANISM: Homo sapien
US-10-301-480-1091533
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-10-301-480-1091533/c
                                                                                                                                                                                                                                                                                                                                             US-10-301-480-478124/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: DNA
                                                                                                                                                                                       δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 7
US-10-301-480-594607
is Sequence 584607
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Wang, David G.

APPLICANT: Wang, David G.

IITLE OF INVENTION: Inter Human Genome
TITLE OF INVENTION: In the Human Genome
TITLE OF INVENTION NUMBER: US/10/301,480
CURRENT APPLICATION NUMBER: US 10/215,598
PRIOR PILING DATE: 2002-08-09
PRIOR PILING DATE: 2002-08-09
PRIOR FILING DATE: 2001-08-10
NUMBER OF SEQ ID NOS: 1226818
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 1208016
LENGTH: 557
TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                          51.5%; Score 20.6; DB 10; Length 535; 74.3%; Pred. No. 87; tive 0; Mismatches 9; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 557;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              167 GATTATTGGTTGCAGAGTCCTGCTTGGTAACTCTT 201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    245 garggregeregraaaaagcreecragacagaerr 279
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              6 GATTCTTGGCGGTAGAGAGCTGCTTGGTCAGACTT 40
                                                                                                                                                                                                                                                                                                                                                                                                                         6 GATTCTTGGCGGTAGAGAGCTGCTTGGTCAGACTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       score 20.6; DE Fred. No. 88; O; Mismatches
PRIOR APPLICATION NUMBER: US 10/215,598
PRIOR FILING DATE: 2002-08-09
PRIOR APPLICATION NUMBER: US 60/311,695
PRIOR PILING DATE: 2001-08-10
NUMBER OF SEQ ID NOS: 1226818
SOFTWARE: PRESEQ for Windows Version 4.0
LENGTH: 535
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 1208016, Application US/10301480 Publication No. US20060057564A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 74.3%;
Matches 26; Conservative (
                                                                                                                                                                                                                                                                                                                                        Best Local Similarity 74.3
Matches 26; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; ORGANISM: Homo sapien
US-10-301-480-594607
                                                                                                                                                                                                                                    ; ORGANISM: Homo sapien
US-10-301-480-624090
                                                                                                                                                                                                                                                                                                                     Query Match
```

ઠે 셤

셤

```
APPLICANT: BATES, Stephen
APPLICANT: BATES, Stephen
APPLICANT: BATES, Stephen
TITLE OF INVENTION: METHODS AND SYSTEMS FOR INFERRING BOVINE TRAITS
TITLE OF INVENTION: METHODS
TITLE OF INVENTION: METHODS
TITLE OF INVENTION: MOMBER: US/10/750,623
CURRENT FAPLICATION NUMBER: US/0/437,482
PRIOR PAPLICATION NUMBER: US 60/437,482
PRIOR APPLICATION NUMBER: US 60/437,482
SPRIOR APPLICATION NUMBER: US 60/437,482
SOFTWARE: PATENT OF SEQ ID NOS: 64922
SOFTWARE: PATENT OF SEQ ID NOS: 64922
SOFTWARE: PATENT OF SEQ ID NOS: 64923
SOFTWARE: PATENT OF SEQ ID NOS: 64923
SEQ ID NO 48123
LENGTH: 1381
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-US-JS-US-A-757544, Application US/09925065A; Bequence 757534, Application US/09925065A; Publication No. US2040181048A1; GEWERAL INFORMATION:

GENERAL INFORMATION:

APPLICANT: Wang, David G.

TITLE OF INVENTION: Nuclectide Polymorphisms in the Human Genome; ITLE REFERENCE: 108827.135

CURRENT APPLICATION NUMBER: US/09/925,065A; CURRENT PILING DATE: 2001-08-08

FRIOR PELICATION NUMBER: US 60/243,096

PRIOR PELICATION NUMBER: US 60/252,147

FRIOR PELICATION NUMBER: US 60/250,092

FRIOR PELICATION NUMBER: US 60/250,092

FRIOR PELICATION NUMBER: US 60/250,092

FRIOR PELICATION NUMBER: US 60/261,766

FRIOR APPLICATION NUMBER: US 60/261,766

FRIOR PELING DATE: 2001-01-16

FRIOR APPLICATION NUMBER: US 60/261,766

FRIOR PELING DATE: 2001-01-16

FRIOR PELING DATE: 2001-01-16

FRIOR PELING DATE: 2001-05-09

NUMBER OF SEQ ID NOS: 957046

SEQ ID NO 757534

LENGTH: 640
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 20.6; DB 8; Length 1381;
Pred. No. 1e+02;
0; Mismatches 9; Indels 0.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 640;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1276 TACAGAAGTTTGGAGGTAGGTAGCTGCTGGTTCAG 1242
1276 TACAGAAGTTTGGAGGTAGGTAGCTGCTGGTTCAG 1242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
50.5%; Score 20.2; DB 6;
Best Local Similarity 75.8%; Pred. No. 1.3e+02;
Matches 25; Conservative 0; Mismatches 8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2 TCCAGATTCTTGGCGGTAGAGAGCTGCTTGGTCAG 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           5 AGATTCTTGGCGGTAGAGAGCTGCTTGGTCAGA 37
                                                                                                                                             Sequence 48123, Application US/10750623
Publication No. US20050287531A1
GENERAL INFORMATION:
APPLICANT: MAI GENOMICS, INC.
APPLICANT: KERR, Richard
APPLICANT: KERR, Richard
APPLICANT: ROSENFELD, David
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; TYPE: DNA
; ORGANISM: Bovine 19866881441129
US-10-750-623-48123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     51.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best Local Similarity 74.3
Matches 26; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; ORGANISM: Homo sapiens US-09-925-065A-757534
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 14
US-09-925-065A-757534/c
                                                                                                                   US-10-750-623-48123/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                   US-09-1925-005A-H1990, Application US/09925065A

Publication No. US20040181048A1

FREMENTIAL INFORMATION:

APPLICANT: Wang, David G.

TITLE OF INVENTION: Identification and Mapping of Single

TITLE OF INVENTION: UNCLEOCIDE OF SOURCE OUR STATE REFERENCE: 108827.135

CURRENT PAPLICATION NUMBER: US 60/255,065A

FRIOR FILING DATE: 2000-10-24

FRIOR FILING DATE: 2000-11-20

FRIOR APPLICATION NUMBER: US 60/250,092

FRIOR APPLICATION NUMBER: US 60/250,092

FRIOR APPLICATION NUMBER: US 60/261,766

FRIOR APPLICATION NUMBER: US 60/289,846

FRIOR FILING DATE: 2001-01-16

FRIOR FILING DATE: 2001-01-16

FRIOR PELING DATE: 2001-05-09

NUMBER OF SEQ ID NOS: 957086

SOFTWARE FREEESEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 48123, Application US/10750185
| Publication No. US20050260603A1
| GENERAL INFORMATION:
| APPLICANT: MAI GENOMICS, INC.
| APPLICANT: MAI GENOMICS, INC.
| APPLICANT: MERK, Richard
| APPLICANT: RERK, Richard
| APPLICANT: RERK, Richard
| APPLICANT: BATES, Stephen
| APPLICANT: BATES, Stephen
| APPLICANT: BATES, Stephen
| APPLICANT: BANTIN, Dennis
| TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
| TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
| TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
| TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
| TITLE OF INVENTION WHEBER: US 60/437,482
| PRIOR PLICATION NUMBER: US 60/437,482
| PRIOR FILING DATE: 2002-12-31
| PRIOR FILING DATE: 2002-12-31
| WUMBER OF SEQ ID NOS: 64922
| SOFTWARE: PATENTIN VETSION 3.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 51.5%; Score 20.6; DB 8; Length 1381; Best Local Similarity 74.3%; Pred. No. 18+02; Matches 26; Conservative 0; Mismatches 9; Indels 0.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 596;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               544 GATAATTTGCAGGAAAGAGCAACTTTGTCAGACTT 578
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        6 GATTCTTGGCGGTAGAGAGCTGCTTGGTCAGACTT 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2 TCCAGATTCTTGGGGGTAGAGGGGCTGCTTGGTCAG 36
49 GATAATTTGCAGGAAAGAGCAACTTTGTCAGACTT 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
51.5%; Score 20.6; D)
Best Local Similarity 74.3%; Pred. No. 89;
Matches 26; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; TYPE: DNA
; ORGANISM: Bovine 19866881441129
US-10-750-185-48123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; ORGANISM: Homo sapiens
US-09-925-065A-411990
                                                                                                                      US-09-925-065A-411990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 12
US-10-750-185-48123/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQ ID NO 48123
LENGTH: 1381
```

Matches

ઠે 셤

ö

Gaps

ö

ö

Gaps

583 AGATGTTAGCAGGAAGAGAGCTGCTGGGGCAGA 551

셤

```
Query Match 50.5%; Score 20.2; DB 14; Length 1073; Best Local Similarity 75.8%; Pred. No. 1.5e+02; Matches 25; Conservative 0; Mismatches 8; Indels 0;
                                                                                                                                                                                                                                    GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Liu, Chenghua
APPLICANT: Asundi, Vinod
APPLICANT: Gian, Xiachong B.
APPLICANT: Qian, Xiachong B.
APPLICANT: Wehrman, Tom
APPLICANT: Wehrman, Tom
APPLICANT: Cao, Yi-Cheng
APPLICANT: Dranacc, Radoje T.
TITLE OF INVENTION: NOWBER: US/11/000,463
CURRENT APPLICATION NUMBER: 09/491,265
PRIOR PILING DATE: 2001-01-025
PRIOR PLILNG DATE: 2001-01-03
PRIOR PLILNG DATE: 2000-01-12
PRIOR APPLICATION NUMBER: 09/491,404
PRIOR PLILNG DATE: 2000-00-03
PRIOR PLING DATE: 2000-00-03
PRIOR PR
RESULT 15
US-11-000-463-507/c
is Sequence 507, Application US/11000463
is Publication No. US20050266423A1
igeneral information:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-000-463-507
```

691 AGATGTTAGCAGGAGAGAGCTGCTGGGGCAGA 659 셤

5 AGATTCTTGGCGGTAGAGAGCTGCTTGGTCAGA 37

ð

ö

Gaps ö

Search completed: April 18, 2006, 20:01:33 Job time : 353 secs

This Page Blank (uspto)